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Research Article

Taxonomy and phylogeny of Auriculariales (Agaricomycetes, Basidiomycota) with descriptions of four new species from south-western China

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Abstract

The wood-inhabiting fungi play an integral role in wood degradation and the cycle of matter in the ecological system. They are considered as the "key player" in wood decomposition, because of their ability to produce lignocellulosic enzymes that break down woody lignin, cellulose and hemicellulose. In the present study, four new wood-inhabiting fungal species, *Adustochaete albomarginata*, *Ad. punctata*, *Alloexidiopsis grandinea* and *Al. xantha* collected from southern China, are proposed, based on a combination of morphological features and molecular evidence. *Adustochaete albomarginata* is characterised by resupinate basidiomata with cream to buff, a smooth, cracked, hymenial surface, a monomitic hyphal system with clamped generative hyphae and subcylindrical to allantoid basidiospores (12–17.5 × 6.5–9 µm). *Adustochaete punctata* is characterised by resupinate basidiomata with cream, a smooth, punctate hymenial surface, a monomitic hyphal system with clamped generative hyphae and subcylindrical to allantoid basidiospores (13.5–18 × 6–8.2 µm). *Alloexidiopsis grandinea* is characterised by resupinate basidiomata with buff to slightly yellowish, a grandinioid hymenial surface, a monomitic hyphal system with clamped generative hyphae and allantoid basidiospores (10–12.3 × 5–5.8 µm). Additionally, *Alloexidiopsis xantha* is characterised by resupinate basidiomata with cream to slightly buff, a smooth hymenial surface, a monomitic hyphal system with clamped generative hyphae and subcylindrical to allantoid basidiospores measuring 20–24 × 5–6.2 µm. Sequences of the internal transcribed spacers (ITS) and the large subunit (nrLSU) of the nuclear ribosomal DNA (rDNA) markers of the studied samples were generated. Phylogenetic analyses were performed with the Maximum Likelihood, Maximum Parsimony and Bayesian Inference methods. The phylogram, based on the ITS+nLSU rDNA gene regions, revealed that four new species were assigned to the genera *Adustochaete* and *Alloexidiopsis* within the order Auriculariales, individually. The phylogenetic tree inferred from the ITS sequences highlighted that *Ad. albomarginata* was retrieved as a sister to *Ad. yunnanensis* and the species *Ad. punctata* was sister to *Ad. rava*. The topology, based on the ITS sequences, showed that *Al. grandinea* was retrieved as a sister to *Al. schistacea* and the taxon *Al. xantha* formed a monophyletic lineage. Furthermore, two identification keys to *Adustochaete* and *Alloexidiopsis* worldwide are provided.

Key words: Biodiversity, molecular systematics, taxonomy, wood-inhabiting fungi, Yunnan Province

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Introduction

In forest ecosystems, fungi play an essential ecological role to drive carbon cycling in forest soils, mediate mineral nutrition of plants and alleviate carbon limitations (Tedersoo et al. 2014). The fungal order Auriculariales is a group mainly composed of wood-inhabiting fungi in Agaricomycetes Doweld (Basidiomycota) (Hibbett et al. 2007). The type genus of this order is *Auricularia* Bull., in which several other gelatinous genera *Exidia* Fr., *Guepinia* Fr. and *Pseudohydnum* P. Karst., comprise important edible and medicinal fungi (Wu et al. 2019; Liu et al. 2022). Therefore, interest in species diversity in gelatinous genera has increased significantly in recent years (Chen et al. 2020; Shen and Fan 2020; Ye et al. 2020; Wang and Thorn 2021; Wu et al. 2021; Tohtirjap et al. 2023).

Contrary to the gelatinous genera, most species in the order Auriculariales are tough, include saprophytic species with resupinate, effused-reflexed, hydnoid, cerebriform, coralloid or pileate basidiomata (Wells and Bandoni 2001; Miettinen et al. 2012; Hibbett et al. 2014; Malysheva and Spirin 2017; Alvarenga et al. 2019; Spirin et al. 2019a, 2019b; Liu et al. 2022; Tohtirjap et al. 2023). Species with the stereoid basidiocarps are widely distributed in many orders of the Agaricomycetes, although they are certainly a minority in the order Auriculariales (Malysheva and Spirin 2017).

The genus *Adustochaete* Alvarenga & K.H. Larss. was erected by Alvarenga and Larsson and typed by the taxon *Ad. rava* Alvarenga & K.H. Larss. It is characterised by the resupinate basidiomata, spiny or tuberculate hymenophore, a monomitic hyphal structure with clamp connections on generative hyphae, present cystidia and hyphidia, ellipsoid-ovoid to obconical basidia, cylindrical to broadly cylindrical, straight or curved basidiospores (Alvarenga et al. 2019). The genus *Alloexidiopsis* L.W. Zhou & S.L. Liu is typified by *Al. schistacea* L.W. Zhou & S.L. Liu, which is c characterised by annual, resupinate basidiomata, smooth or with sterile spines hymenophore, a monomitic hyphal structure with clamp connections on generative hyphae, present cystidia and hyphidia, ellipsoid to ovoid, septate basidia, and cylindrical to broadly cylindrical, slightly curved (allantoid) basidiospores (Liu et al. 2022). Based on the MycoBank database (http://www.mycobank.org, accessed on 25 July 2024) and the Index Fungorum (http://www.indexfungorum.org, accessed on 25 July 2024), the genera *Adustochaete* and *Alloexidiopsis* have registered four and six species, respectively (Alvarenga et al. 2019; Guan et al. 2020; Hyde et al. 2020; Li et al. 2022a, 2022b; Li and Zhao 2022; Liu et al. 2022; Dong et al. 2024).

Classification of the kingdom of fungi has been updated continuously, based on the frequent inclusion of data from DNA sequences in many phylogenetic studies (Wijayawardene et al. 2020, 2022). Based on the early embrace of molecular systematics by mycologists, both the discovery and classification of fungi, amongst the more basal branches of the tree, are now coming to light from genomic analyses and environmental DNA surveys that have been conducted (James et al. 2020). Based on both the morphological and phylogenetic evidence, the generic concepts of *Eichleriella* Bres., *Hirneolina* (Pat.) Bres. and *Tremellochaete* Raitv. were revised, in which Malysheva and Spirin (2017) proposed that the genus *Heteroradulum* Lloyd ex Spirin and Malysheva was validated. The genus *Eichleriella* was accepted to be a monophyletic genus,

while both genera *Exidiopsis* (Bref.) Möller and *Heterochaete* Pat. seemed to be synonymous, with priority given to the latter genus (Malysheva and Spirin 2017; Alvarenga et al. 2019; Alvarenga and Gibertoni 2021). However, certain species of *Exidiopsis*, even sequenced ones such as *E. calcea* (Pers.) K. Wells and *E. grisea* (Bres.) Bourdot & Maire, still have no appropriate placement at the generic level (Malysheva and Spirin 2017; Li et al. 2022a; Liu et al. 2022).

In recent years, the species diversity of the resupinate Auriculariales have been described or better defined using morphological and molecular analyses and the results showed the hidden diversity of this group and several corticioid genera, for example, *Adustochaete*, *Alloexidiopsis*, *Amphistereum* Spirin & Malysheva, *Crystallodon* Alvarenga, *Heteroradulum*, *Metulochaete* Alvarenga, *Proterochaete* Spirin & Malysheva and *Sclerotrema* Spirin & Malysheva, which have been established and described, based on the morphological and phylogenetic studies (Malysheva and Spirin 2017; Alvarenga et al. 2019; Spirin et al. 2019a, 2019b; Alvarenga and Gibertoni 2021; Liu et al. 2022).

During investigations on wood-inhabiting fungi in the Yunnan-Guizhou Plateau, China, many specimens were collected. To clarify the placement and relationships of these specimens, we carried out a phylogenetic and taxonomic study, based on the ITS+nLSU and ITS sequences. These specimens were assigned to the genera *Adustochaete* and *Alloexidiopsis* within the order Auriculariales. Therefore, four new species *Ad. albomarginata*, *Ad. punctata*, *Al. grandinea* and *Al. xantha* are proposed with description and illustrations, based on the morphological characteristics and phylogenetic analyses.

Materials and methods

Sample collection and herbarium specimen preparation

The fresh fruiting bodies were collected on the fallen angiosperm branches from Dali, Dehong, Diqing, Lincang and Zhaotong of Yunnan Province, China. The samples were photographed in situ and fresh macroscopic details were recorded. Photographs were recorded by a Nikon D7100 camera. All the photos were focus-stacked using Helicon Focus software. Macroscopic details were recorded and transported to a field station where the fruit body was dried on an electronic food dryer at 45 °C. Once dried, the specimens were sealed in an envelope and zip-lock plastic bags and labelled (Zhang et al. 2024). The dried specimens were deposited in the Herbarium of the Southwest Forestry University (SWFC), Kunming, Yunnan Province, China.

Morphology

The macromorphological descriptions were based on field notes and photos captured in the field and lab. The colour terminology follows Petersen (1996). The micromorphological data were obtained from the dried specimens after observation under a light microscope with a magnification of 10 × 100 oil (Zhao et al. 2023). Sections mounted in 5% potassium hydroxide (KOH) and 2% phloxine B dye ($C_{20}H_2Br_4C_{l4}Na_2O_5$) and we also used other reagents, including Cotton Blue and Melzer's reagent to observe micromorphology following Wu et al. (2022b). To show the variation in spore sizes, 5% of measurements were

excluded from each end of the range and shown in parentheses. At least thirty basidiospores from each specimen were measured. Stalks were excluded from basidia measurements and the hilar appendage was excluded from basidiospores measurements. The following abbreviations are used: KOH = 5% potassium hydroxide water solution, CB– = acyanophilous, IKI– = both inamyloid and non-dextrinoid, L = mean spore length (arithmetic average for all spores), W = mean spore width (arithmetic average for all spores), Q = variation in the L/W ratios between the specimens studied, Q_m represented the average Q of basidiospores measured ± standard deviation and n = a/b (number of spores (a) measured from given number (b) of specimens).

Molecular phylogeny

The CTAB rapid plant genome extraction kit-DN14 (Aidlab Biotechnologies Co., Ltd., Beijing, China) was used to obtain genomic DNA from the dried specimens according to the manufacturer's instructions. The ITS region was amplified with ITS5 and ITS4 primers (White et al. 1990). The nLSU region was amplified with the LR0R and LR7 (Vilgalys and Hester 1990; Rehner and Samuels 1994). The PCR procedure for ITS was as follows: initial denaturation at 95 °C for 3 min, followed by 35 cycles at 94 °C for 40 s, 58 °C for 45 s and 72 °C for 1 min and a final extension of 72 °C for 10 min. The PCR procedure for nLSU was as follows: initial denaturation at 94 °C for 1 min, followed by 35 cycles at 94 °C for 30 s, 48 °C for 1 min and 72 °C for 1.5 min and a final extension of 72 °C for 10 min. The PCR products were purified and sequenced at Kunming Tsingke Biological Technology Limited Company (Yunnan Province, P.R. China). The newly-generated sequences were deposited in NCBI GenBank (Table 1).

The sequences were aligned in MAFFT v. 7 (Katoh et al. 2019) using the G-INS-i strategy. The alignment was adjusted manually using AliView v. 1.27 (Larsson 2014). The dataset was aligned first and then the sequences of ITS+nLSU were combined with Mesquite v. 3.51. The combined ITS+nLSU sequences and ITS datasets were used to infer the position of the new species and related species. The sequence of *Sistotrema brinkmannii* (Bres.) J. Erikss. obtained from GenBank was used as an outgroup to root trees in the ITS+nLSU analysis (Fig. 1) in the order Auriculariales (Tohtirjap et al. 2023). The sequence of *Amphistereum leveilleanum* (Berk. & M.A. Curtis) Spirin & Malysheva obtained from GenBank was used as an outgroup to root trees in the ITS analysis in the genus *Adustochaete* (Fig. 2). The sequence of *Heteroradulum kmetii* (Bres.) Spirin & Malysheva obtained from GenBank was used as an outgroup to root trees in the ITS analysis in the genus *Alloexidiopsis* (Fig. 3).

Maximum Parsimony (MP), Maximum Likelihood (ML) and Bayesian Inference (BI) analyses were applied to the combined three datasets following a previous study (Zhao and Wu 2017) and the tree construction procedure was performed in PAUP* v. 4.0b10 (Swofford 2002). All of the characters were equally weighted and gaps were treated as missing data. Using the heuristic search option with TBR branch swapping and 1000 random sequence additions, trees were inferred. Maxtrees were set to 5000, branches of zero length were collapsed and all parsimonious trees were saved. Clade robustness was assessed using bootstrap (BT) analysis with 1000 replicates (Felsenstein 1985). Descriptive tree statistics, tree length (TL), the consistency index (CI),

the retention index (RI), the rescaled consistency index (RC) and the homoplasy index (HI) were calculated for each maximum parsimonious tree generated. The multiple sequence alignment was also analysed using Maximum Likelihood (ML) in RAxML-HPC2 on XSEDE v. 8.2.8 with default parameters (Miller et al. 2012). Branch support (BS) for ML analysis was determined by 1000 bootstrap replicates.

jModelTest v. 2 (Darriba et al. 2012) was used to determine the best-fit evolution model for each dataset for the purposes of Bayesian Inference (BI), which was performed using MrBayes 3.2.7a with a GTR+I+G model of DNA substitution and a gamma distribution rate variation across sites (Ronquist et al. 2012). The first one-quarter of all the generations were discarded as burn-in. The majority-rule consensus tree of all the remaining trees was calculated. Branches were considered significantly supported if they received a Maximum Likelihood bootstrap value (BS) of > 70%, a Maximum Parsimony bootstrap value (BT) of > 70% or Bayesian Posterior Probabilities (BPP) of > 0.95.

Results

Sequence similarity search

The results of BLAST queries in NCBI, based on ITS and nLSU separately, showed the sequences producing significant alignment descriptions:

Adustochaete albomarginata: in ITS BLAST results, *Ad. rava*, *Exidia saccharina* Fr., *Ea. qinghaiensis* S.R. Wang & Thorn, *Ad. nivea* Alvarenga and *Exidiopsis mucedinea* (Pat.) K. Wells were found as the top ten taxa (maximum record descriptions: Max score 830; Total score 830; Query cover 96%; E value 0.0; Ident 92.93%). In nLSU BLAST results, *Alloexidiopsis yunnanensis* (C.L. Zhao) L.W. Zhou & S.L. Liu, *Auricularia asiatica* Bandara & K.D. Hyde, *Au. brasiliana* Y.C. Dai & F. Wu and *Steccherinum nandinae* (F. Wu, P. Du & X.M. Tian) Z.B. Liu, Y.C. Dai & Jing Si were found as the top ten taxa (maximum record descriptions: Max score 2398; Total score 2398; Query cover 98%; E value 0.0; Ident 98.60%).

Adustochaete punctata: in ITS BLAST results, *Ad. rava*, *Ad. nivea*, *Exidiopsis mucedinea* and *Exidia candida* Lloyd were found as the top ten taxa (maximum record descriptions: Max score 959; Total score 959; Query cover 96%; E value 0.0; Ident 96.74%). In nLSU BLAST results, *Ad. rava*, *Ad. yunnanensis* Y.F. Li & C.L. Zhao., *Auricularia thailandica* Bandara & K.D. Hyde, *Au. scissa* Looney, Birkebak & Matheny, *Au. nigricans* (Sw.) Birkebak, Looney & Sánchez-García and *Alloexidiopsis yunnanensis* were found as the top ten taxa (maximum record descriptions: Max score 2464; Total score 2464; Query cover 98%; E value 0.0; Ident 99.34%).

Alloexidiopsis grandinea: in ITS BLAST results, *Ad. nivea* and *Al. schistacea* were found as the top ten taxa (maximum record descriptions: Max score 861; Total score 861; Query cover 91%; E value 0.0; Ident 94.94%).

Alloexidiopsis xantha: in ITS BLAST results, *Al. sinensis* J.H. Dong & C.L. Zhao was found as the top ten taxa (maximum record descriptions: Max score 832; Total score 832; Query cover 98%; E value 0.0; Ident 92.42%). In nLSU BLAST results, *Al. sinensis* and *Al. yunnanensis* were found as the top ten taxa (maximum record descriptions: Max score 2457; Total score 2457; Query cover 99%; E value 0.0; Ident 99.05%).

Table 1. List of species, specimens, and GenBank accession number of sequences used in this study.

Species Name	Sample No.	GenBank Accession No.		Country	References
		ITS	nLSU		
Adustochaete albomarginata	**CLZhao 22774 ***	**PP852049**	**PP849033**	**China**	**Present study**
Adustochaete interrupta	LR 23435	MK391518	MK391527	Brazil	Alvarenga et al. (2019)
Adustochaete nivea	RLMA 531	MN165954	MN165989	USA	Liu et al. (2022)
Adustochaete punctata	**CLZhao 29669**	**PP852050**	—	**China**	**Present study**
Adustochaete punctata	**CLZhao 29671**	**PP852051**	**PP849034**	**China**	**Present study**
Adustochaete punctata	**CLZhao 29675 ***	**PP852052**	**PP849035**	**China**	**Present study**
Adustochaete punctata	**CLZhao 29685**	**PP852053**	**PP849036**	**China**	**Present study**
Adustochaete punctata	**CLZhao 29686**	**PP852054**	**PP849037**	**China**	**Present study**
Adustochaete punctata	**CLZhao 29706**	**PP852055**	—	**China**	**Present study**
Adustochaete punctata	**CLZhao 29710**	**PP852056**	**PP849038**	**China**	**Present study**
Adustochaete punctata	**CLZhao 29711**	**PP852057**	**PP849039**	**China**	**Present study**
Adustochaete rava	RC 841	MK391516	—	Brazil	Alvarenga et al. (2019)
Adustochaete rava	KHL 15526	MK391517	MK391526	Brazil	Alvarenga et al. (2019)
Adustochaete yunnanensis	CLZhao 8212	MZ911964	MZ950629	China	Li and Zhao (2022)
Adustochaete yunnanensis	CLZhao 4671	MZ911965	—	China	Li and Zhao (2022)
Adustochaete yunnanensis	CLZhao 4401	MZ911966	MZ950630	China	Li and Zhao (2022)
Alloexidiopsis australiensis	LWZ 20180514-18	OM801934	OM801919	China	Liu et al. (2022)
Alloexidiopsis australiensis	LWZ 20180513-22	OM801933	OM801918	China	Liu et al. (2022)
Alloexidiopsis calcea	LWZ 20180904-14	OM801935	OM801920	China	Liu et al. (2022)
Alloexidiopsis calcea	MW 331	AF291280	AF291326	Germany	Weiß and Oberwinkler (2001)
Alloexidiopsis grandinea	**CLZhao 33798 ***	**PP852058**	—	**China**	**Present study**
Alloexidiopsis grandinea	**CLZhao 34279**	**PP852059**	—	**China**	**Present study**
Alloexidiopsis nivea	CLZhao 11204	MZ352947	MZ352938	China	Li et al. (2022a)
Alloexidiopsis nivea	CLZhao 11210	MZ352948	MZ352939	China	Li et al. (2022a)
Alloexidiopsis schistacea	LWZ 20200819-21a	OM801939	OM801932	China	Liu et al. (2022)
Alloexidiopsis xantha	**CLZhao 25093 ***	**PP852060**	**PP849040**	**China**	**Present study**
Alloexidiopsis yunnanensis	CLZhao 8106	MT215569	MT215565	China	Guan et al. (2020)
Alloexidiopsis yunnanensis	CLZhao 4023	MT215568	MT215564	China	Guan et al. (2020)
Amphistereum leveilleanum	FP-106715	KX262119	KX262168	USA	Malysheva and Spirin (2017)
Amphistereum schrenkii	HHB 8476	KX262130	KX262178	USA	Malysheva and Spirin (2017)
Aporpium caryae	Miettinen 14774	JX044145	—	Finland	Miettinen et al. (2012)
Aporpium caryae	WD 2207	AB871751	AB871730	Japan	Sotome et al. (2014)
Auricularia auricula-judae	JT 04	KT152099	KT152115	UK	Tohtirjap et al. (2023)
Auricularia cornea	Dai 13621	MZ618936	MZ669905	China	Tohtirjap et al. (2023)
Auricularia polytricha	TUFC 12920	AB871752	AB871733	Japan	Sotome et al. (2014)
Auricularia tibetica	Dai 13336	MZ618943	MZ669915	China	Tohtirjap et al. (2023)
Bourdotia galzinii	Otto MiettinenX3067	MG757511	MG757511	Spain	Malysheva et al. (2018)
Crystallodon subgelatinosum	RC 1609-URM93444	MN475884	MN475888	Brazil	Alvarenga and Gibertoni (2021)
Crystallodon subgelatinosum	TBG BF-18001-URM93445	MN475885	MN475889	Brazil	Alvarenga and Gibertoni (2021)

Species Name	Sample No.	GenBank Accession No.		Country	References
		ITS	nLSU		
Ductifera sucina	KW3886	AY509551	AY509551	Canada	Liu et al. (2022)
Eichleriella bactriana	TAAM 55071	KX262121	KX262170	Russia	Malysheva and Spirin (2017)
Eichleriella crocata	TAAM 101077	KX262100	KX262147	Russia	Malysheva and Spirin (2017)
Eichleriella leucophaea	Barsukova LE 303261	KX262111	KX262161	Russia	Malysheva and Spirin (2017)
Eichleriella tenuicula	ValCB 1	MK391515	MK391525	Brazil	Alvarenga et al. (2019)
Elmerina cladophora	Miettinen 14314	MG757509	MG757509	Indonesia	Malysheva et al. (2018)
Elmerina sclerodontia	Miettinen 16431	MG757512	MG757512	Malaysia	Malysheva et al. (2018)
Exidia glandulosa	YC Dai 21232	MT663362	MT664781	China	Wu et al. (2020)
Exidia glandulosa	YC Dai 21233	MT663363	MT664782	China	Wu et al. (2020)
Exidia pithya	MW 313	AF291275	AF291321	Germany	Weiß and Oberwinkler (2001)
Grammatus labyrinthinus	Yuan 1600	KM379139	KM379140	China	Alvarenga et al. (2019)
Grammatus semis	OM10618	KX262146	KX262194	China	Malysheva and Spirin (2017)
Heteroradulum adnatum	LR 23453	KX262116	KX262165	Mexico	Tohtirjap et al. (2023)
Heteroradulum kmetii	VS 6466	KX262104	KX262152	Russia	Malysheva and Spirin (2017)
Hyalodon piceicola	Spirin 2689	MG735414	MG735422	Russia	Spirin et al. (2019a)
Hyalodon piceicola	Spirin 11063	MG735415	MG735423	Russia	Spirin et al. (2019a)
Mycostilla vermiformis	Spirin 11330	MG735417	MG735425	Russia	Spirin et al. (2019a)
Mycostilla vermiformis	OF 188059	MG735418	—	Russia	Spirin et al. (2019a)
Myxarium cinnamomescens	OF160494	KY801882	KY801909	Russia	Spirin et al. (2018)
Myxarium grilletii	VS9016	MK098896	MK098944	Russia	Spirin et al. (2019b)
Myxarium hyalinum	TL2012 443455	KY801880	KY801907	Russia	Spirin et al. (2018)
Myxarium legonii	VS 8986	MK098899	MK098947	Russia	Spirin et al. (2019b)
Protodaedalea foliacea	Miettinen 13 054	MG757507	MG757507	Finland	Malysheva et al. (2018)
Protodaedalea hispida	Spirin 5139	MG757510	MG757510	Finland	Malysheva et al. (2018)
Protodontia africana	AS 171126 1104	MK098978	MK098973	Russia	Spirin et al. (2019b)
Protohydnum cartilagineum	SP 467240	MG735419	MG735426	Russia	Malysheva et al. (2018)
Protomerulius dubius	VS 3019	MK484041	MK480553	Russia	Spirin et al. (2019a)
Protomerulius minor	KHL 15937	MK484060	MK480569	Russia	Spirin et al. (2019a)
Protomerulius substuppeus	O 19171	JX134482	JQ764649	China	Spirin et al. (2019a)
Pseudohydnum gelatinosum	F14063	AF384861	AF384861	Canada	Weiß and Oberwinkler (2001)
Pseudohydnum gelatinosum	AFTOL ID1875	DQ520094	DQ520094	Germany	Lutzoni et al. (2004)
Stypellopsis farlowii	Larsson 12337	MG857095	MG857099	Russia	Spirin et al. (2018)
Stypellopsis hyperborea	J Norden 9751	MG857097	MG857101	Russia	Spirin et al. (2018)
Tremellochaete atlantica	URM90199	MG594381	MG594383	Brazil	Alvarenga et al. (2019)
Tremellochaete japonica	TAA 42689	AF291274	AF291320	Russia	Weiß and Oberwinkler (2001)
Tremiscus helvelloides	AFTOL ID1680	DQ520100	DQ520100	Germany	Lutzoni et al. (2004)
Sistotrema brinkmannii	isolate 236	JX535169	JX535170	Netherlands	Alvarenga and Gibertoni (2021)

New species is shown in bold; * is shown type material, holotype.

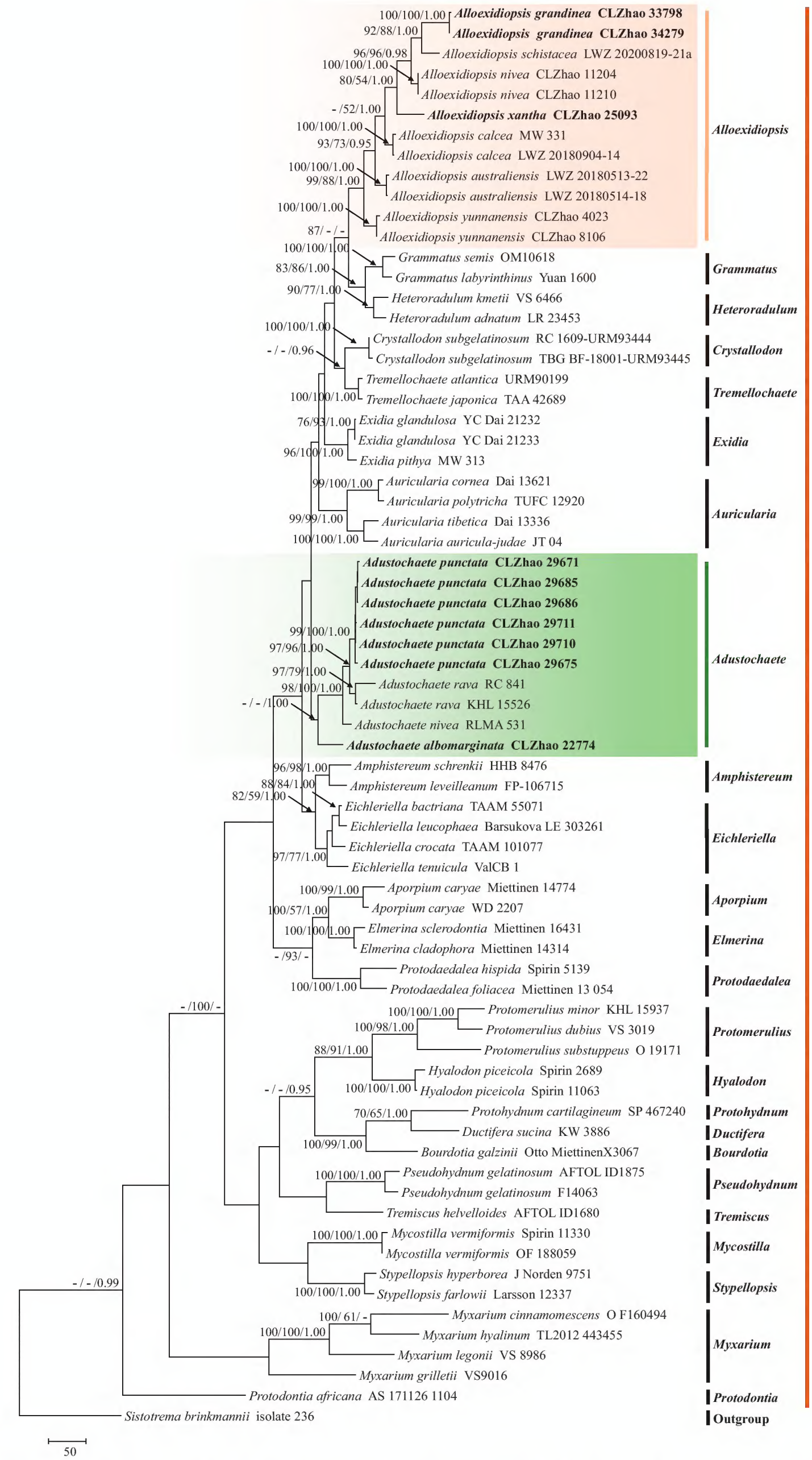

Figure 1. Maximum parsimony strict consensus tree illustrating the phylogeny of *Adustochaete* and *Alloxidiopsis* and related genera in the order Auriculariales, based on ITS+nLSU sequences. Branches are labelled with Maximum Likelihood bootstrap value ≥ 70%, parsimony bootstrap value ≥ 50% and Bayesian posterior probabilities ≥ 0.95.

The aligned dataset comprised 70 specimens representing 53 species. Four Markov chains were run for two runs from random starting trees, each for two million generations for the combine ITS+nLSU (Fig. 1) dataset with trees and parameters sampled every 1000 generations. The dataset had an aligned length of 2333 characters, of which 1301 characters are constant, 368 are variable and parsimony uninformative and 664 are parsimony informative. Maximum parsimony analysis yielded 120 equally parsimonious trees (TL = 4342, CI = 0.4000, HI = 0.6000, RI = 0.5288 and RC = 0.2115). The best model for the ITS+nLSU dataset, estimated and applied in the Bayesian analysis, was SYM+I+G. Both Bayesian analysis and ML analysis resulted in a similar topology to MP analysis with an average standard deviation of split frequencies = 0.008542 (BI) and the effective sample size (ESS) for Bayesian analysis across the two runs is double of the average ESS (avg. ESS) = 395.5.

The aligned dataset comprised 17 specimens representing seven species. Four Markov chains were run for two runs from random starting trees, each for 0.5 million generations for the ITS (Fig. 2) dataset with trees and parameters sampled every 1000 generations. The dataset had an aligned length of 522 characters, of which 413 characters are constant, 47 are variable and parsimony uninformative and 62 are parsimony informative. Maximum parsimony analysis yielded four equally parsimonious trees (TL = 161, CI = 0.8075, HI = 0.1925, RI = 0.8306 and RC = 0.6707). The best model for the ITS dataset, estimated and applied in the Bayesian analysis, was SYM+G. Both Bayesian analysis and ML analysis resulted in a similar topology to MP analysis with an average standard deviation of split frequencies = 0.006786 (BI) and the effective sample size (ESS) for Bayesian analysis across the two runs is double the average ESS (avg. ESS) = 617.

The aligned dataset comprised 13 specimens representing eight species. Four Markov chains were run for two runs from random starting trees, each for 0.3 million generations for the ITS (Fig. 3) dataset with trees and parameters sampled every 1000 generations. The dataset had an aligned length of 562 characters, of which 417 characters are constant, 64 are variable and parsimony uninformative and 81 are parsimony informative. Maximum parsimony analysis yielded two equally parsimonious trees (TL = 218, CI = 0.784, HI = 0.2156, RI = 0.7814 and RC = 0.6129). The best model for the ITS dataset, estimated and applied in the Bayesian analysis, was SYM+G. Both Bayesian analysis and ML analysis resulted in a similar topology to MP analysis with an average standard deviation of split frequencies = 0.007707 (BI) and the effective sample size (ESS) for Bayesian analysis across the two runs is double of the average ESS (avg. ESS) = 639.5.

The phylogram, based on the combined ITS+nLSU sequences (Fig. 1) analysis, showed that four new species *Ad. albomarginata*, *Ad. punctata*, *Al. grandinea* and *Al. xantha* were assigned to the genera *Adustochaete* and *Alloexidiopsis* within the order Auriculariales, individually. The phylogenetic tree, based on ITS sequences (Fig. 2), revealed that *Ad. albomarginata* was retrieved as a sister to *Ad. yunnanensis*. The taxon *Ad. punctata* was sister to *Ad. rava*. The topology, based on the ITS sequences (Fig. 3), revealed that *Al. grandinea* was retrieved as a sister to *Al. schistacea* and the species *Al. xantha* formed a monophyletic lineage.

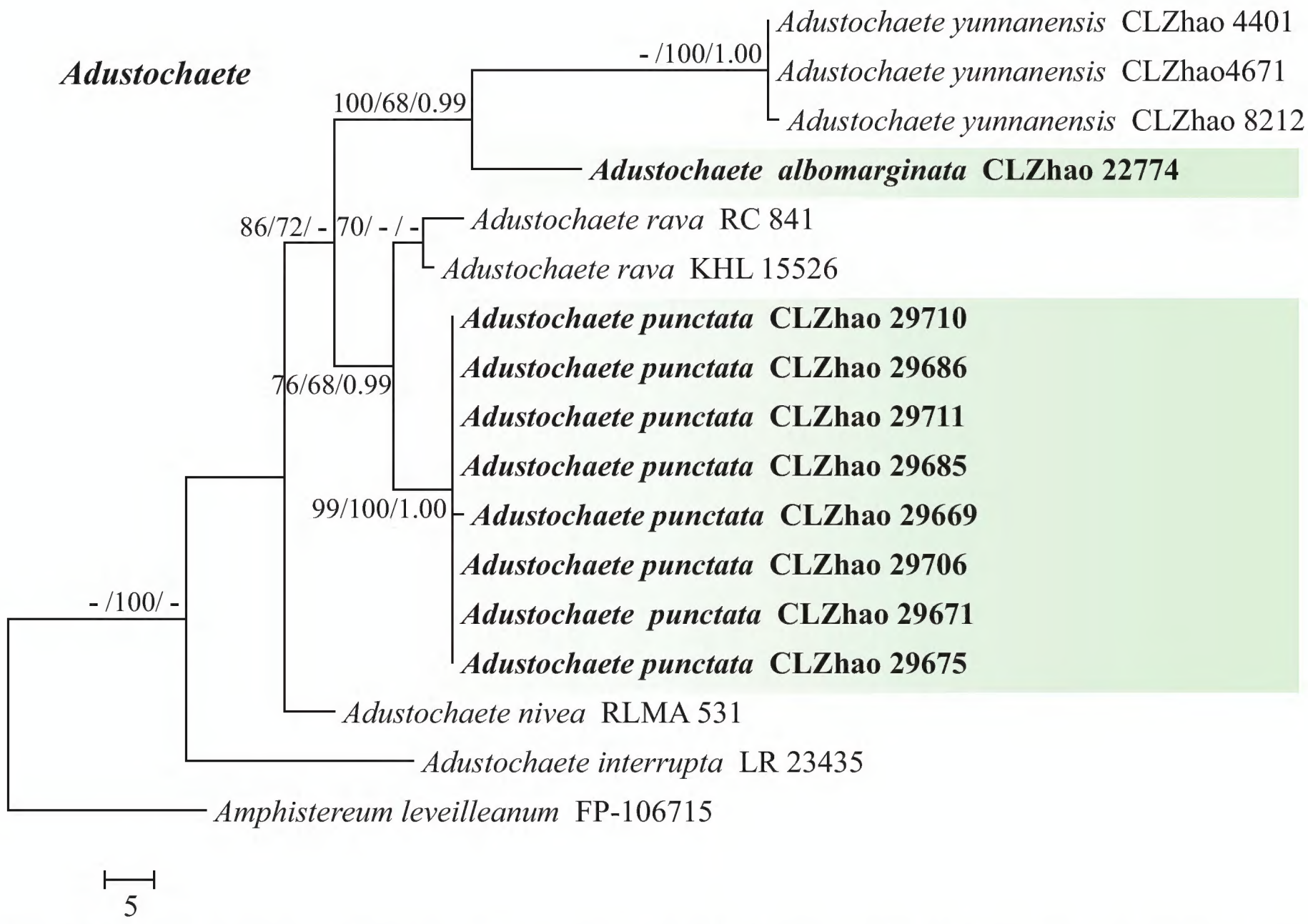

Figure 2. Maximum parsimony strict consensus tree illustrating the phylogeny of the two new species and related genera in the genus *Adustochaete*, based on ITS sequences. Branches are labelled with Maximum Likelihood bootstrap value ≥ 70%, parsimony bootstrap value ≥ 50% and Bayesian posterior probabilities ≥ 0.95.

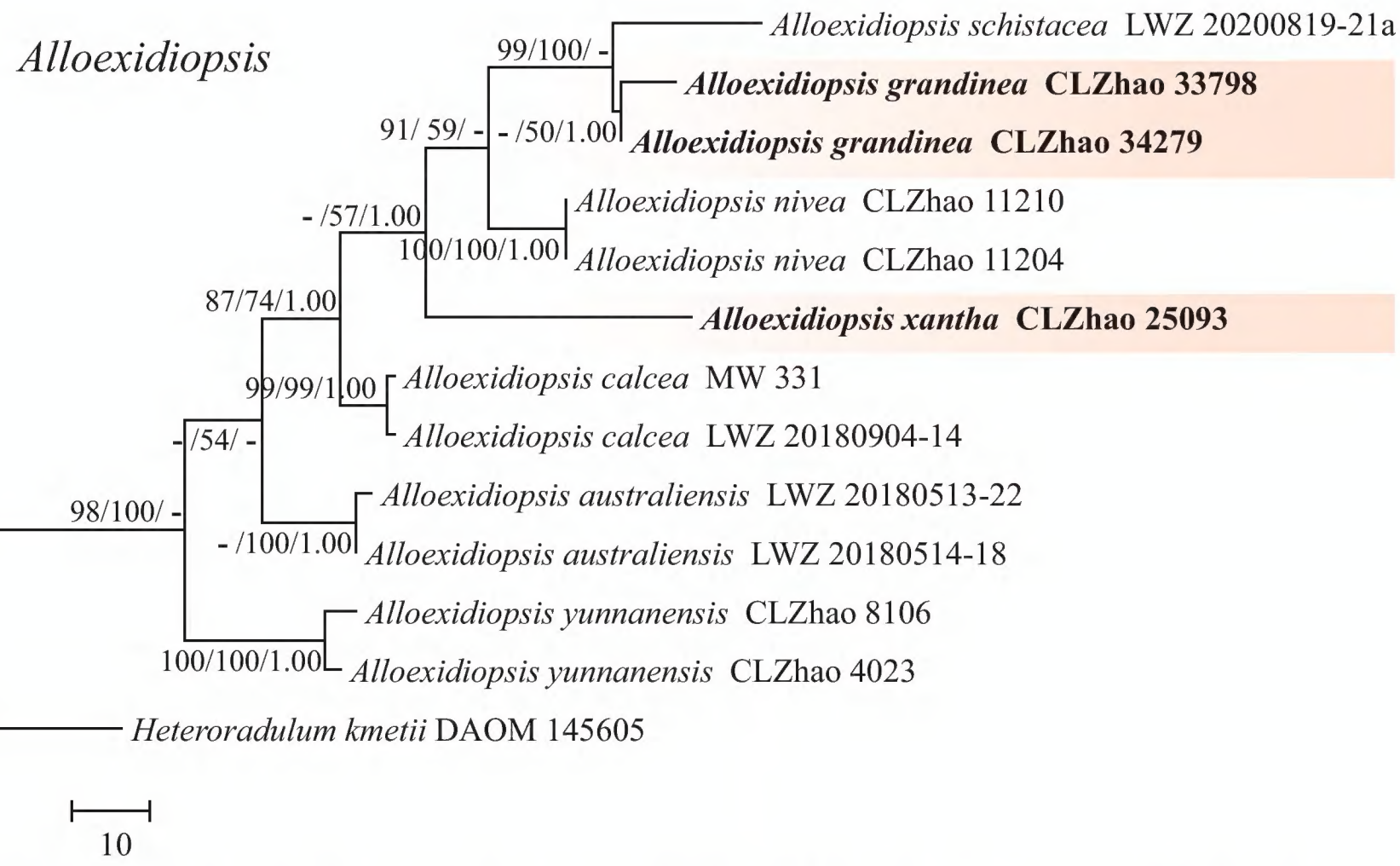

Figure 3. Maximum parsimony strict consensus tree illustrating the phylogeny of the two new species and related genera in the genus *Alloexidiopsis*, based on ITS sequences. Branches are labelled with Maximum Likelihood bootstrap value ≥ 70%, parsimony bootstrap value ≥ 50% and Bayesian posterior probabilities ≥ 0.95.

Taxonomy

Adustochaete albomarginata **J.H Dong & C.L. Zhao, sp. nov.**

MycoBank No: 854168

Figs 4–6

Diagnosis. Differs from other *Adustochaete* species by its soft membranaceous basidiomata with cream to buff, smooth, cracked hymenial surface, a monomitic hyphal system with clamped generative hyphae and subcylindrical to allantoid basidiospores measuring 12–17.5 × 6.5–9 µm.

Holotype. CHINA • Yunnan Province, Dali, Weishan County, Leqiu Town, Zhongyao Village, 25°01'N, 100°19'E, altitude 1910 m, on the fallen branch of angiosperm, leg. C.L. Zhao, 19 July 2022, CLZhao 22774 (SWFC).

Figure 4. Basidiomata of *Adustochaete albomarginata* in general and detailed views (CLZhao 22774, holotype). Scale bars: 1 cm (**A**); 1 mm (**B**).

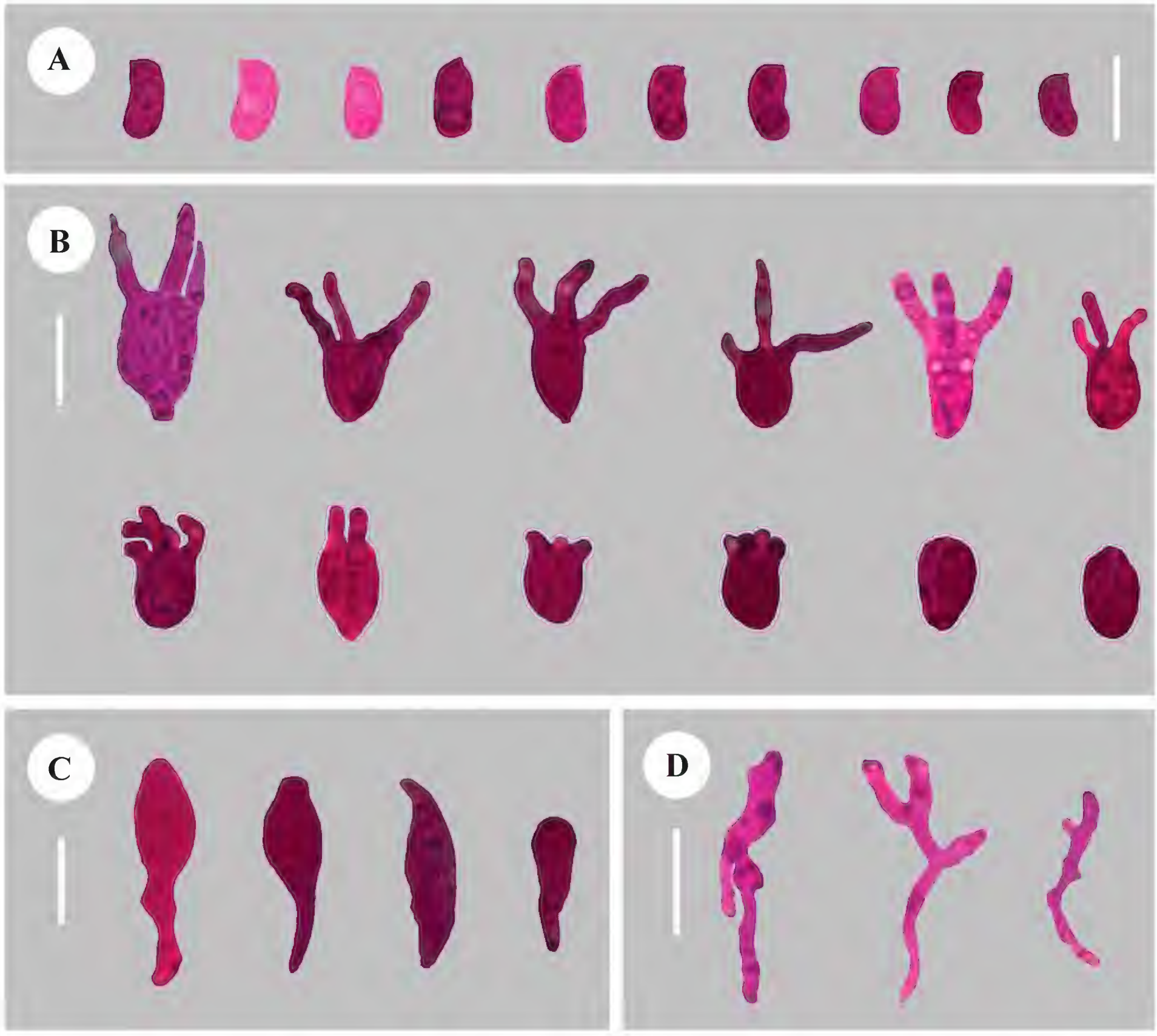

Figure 5. Sections of hymenium of *Adustochaete albomarginata* (holotype, CLZhao 22774) **A** basidiospores **B** basidia **C** cystidia **D** hyphidia. Scale bars: 20 μm (**A–D**); 10 × 100 Oil.

Etymology. *albomarginata* (Latin or Greek origin): referring to the white margin of the basidiomata.

Basidiomata. Annual, resupinate, closely adnate, soft membranaceous, very hard to separate from substrate, without odour or taste when fresh, becoming coriaceous upon drying, up to 5 cm long, 1.5 cm wide, 50–100 μm thick. Hymenial surface smooth, white to cream when fresh, turning to cream to buff upon drying, cracked. Sterile margin white, thinning out, up to 0.5 mm wide.

Hyphal system. Monomitic, generative hyphae with clamp connections, colourless, thin-walled, unbranched, interwoven, 2.5–3.5 μm in diameter; IKI–, CB–, tissues unchanged in KOH. ***Hymenium.*** Cystidia numerous, thin-walled, subclavate to fusiform with an acute or obtuse apex, occasionally sinuous in the basal, 23.5–48.5 × 10–13.5 μm, with a clamp connection at base; cystidioles absent. Hyphidia arising from generative hyphae, nodulose, branched, colourless, thin-walled, 2.5–5 μm in diameter. Basidia ellipsoid to ovoid, longitudinally septate, two to four-celled, 17–24.5 × 11–16.5 μm; basidioles dominant, similar to basidia in shape, but slightly smaller. ***Basidiospores.*** Subcylindrical

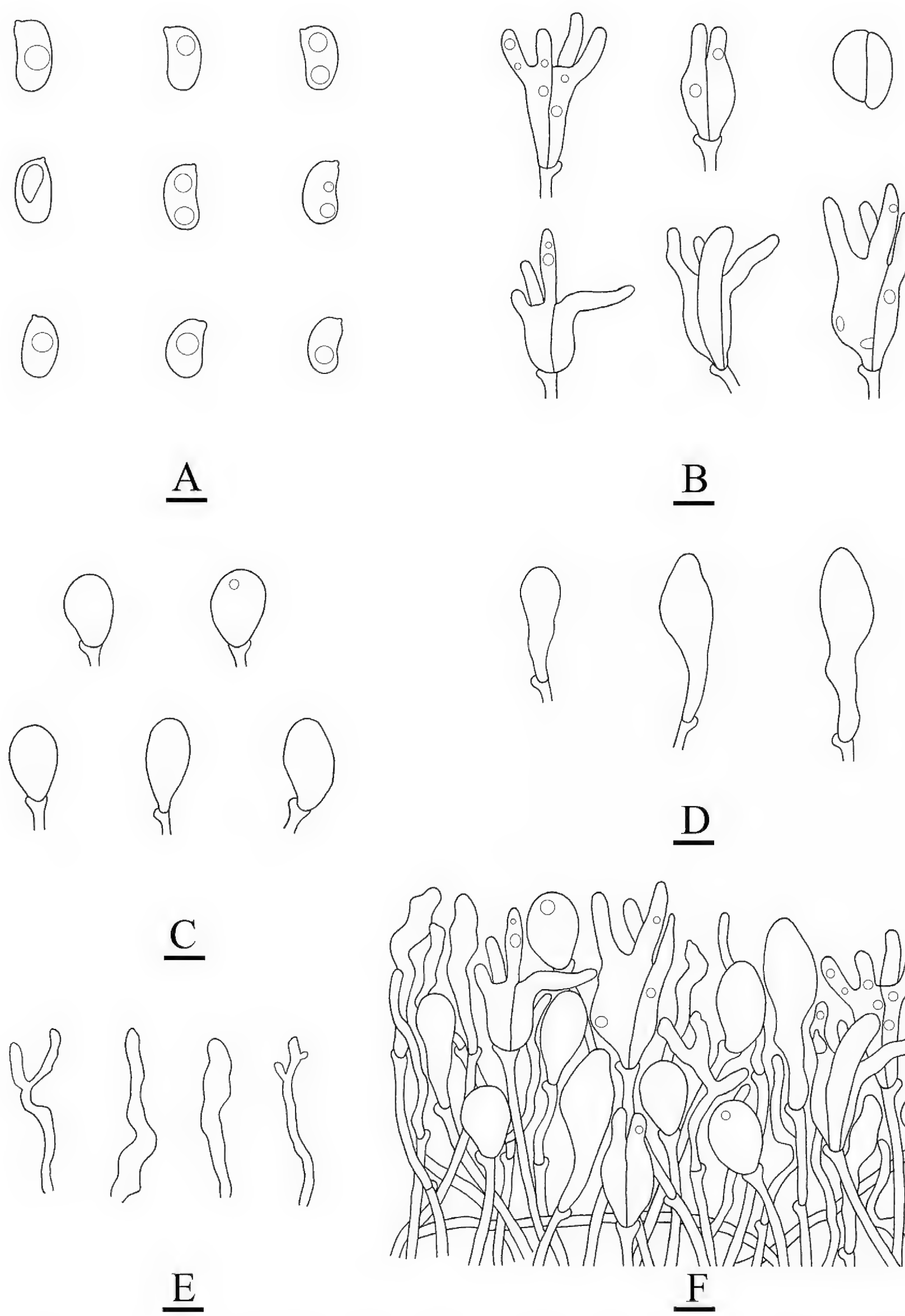

Figure 6. Microscopic structures of *Adustochaete albomarginata* (holotype, CLZhao 22774) **A** basidiospores **B** basidia **C** basidioles **D** cystidia **E** hyphidia **F** part of the vertical section of hymenium. Scale bars: 10 μm (**A–F**).

to allantoid, slightly curved, colourless, smooth, thin-walled, with 1–2 oil drops, IKI–, CB–, (11.5–)12–17.5(–18) × 6.5–9(–9.5) μm, L = 14.66 μm, W = 7.80 μm, Q = 1.72–1.99, Q_m = 1.88 ± 0.08 (n = 30/1).

Adustochaete punctata **J.H Dong & C.L. Zhao, sp. nov.**

MycoBank No: 854170

Figs 7–9

Diagnosis. Differs from other *Adustochaete* species by its membranaceous basidiomata with cream, smooth, punctate hymenial surface, a monomitic hyphal system with clamped generative hyphae and subcylindrical to allantoid basidiospores measuring 13.5–18 × 6–8.2 µm.

Holotype. CHINA • Yunnan Province, Dehong, Yingjiang County, Tongbiguan Provincial Nature Reserve, 23°48'N, 97°38'E, altitude 1500 m, on the fallen branch of angiosperm, leg. C.L. Zhao, 17 July 2023, CLZhao 29675 (SWFC).

Etymology. *punctata* (Latin or Greek origin): referring to the punctate hymenial surface of the specimen.

Figure 7. Basidiomata of *Adustochaete punctata* in general and detailed views (CLZhao 29675, holotype). Scale bars: 1 cm (**A**); 1 mm (**B**).

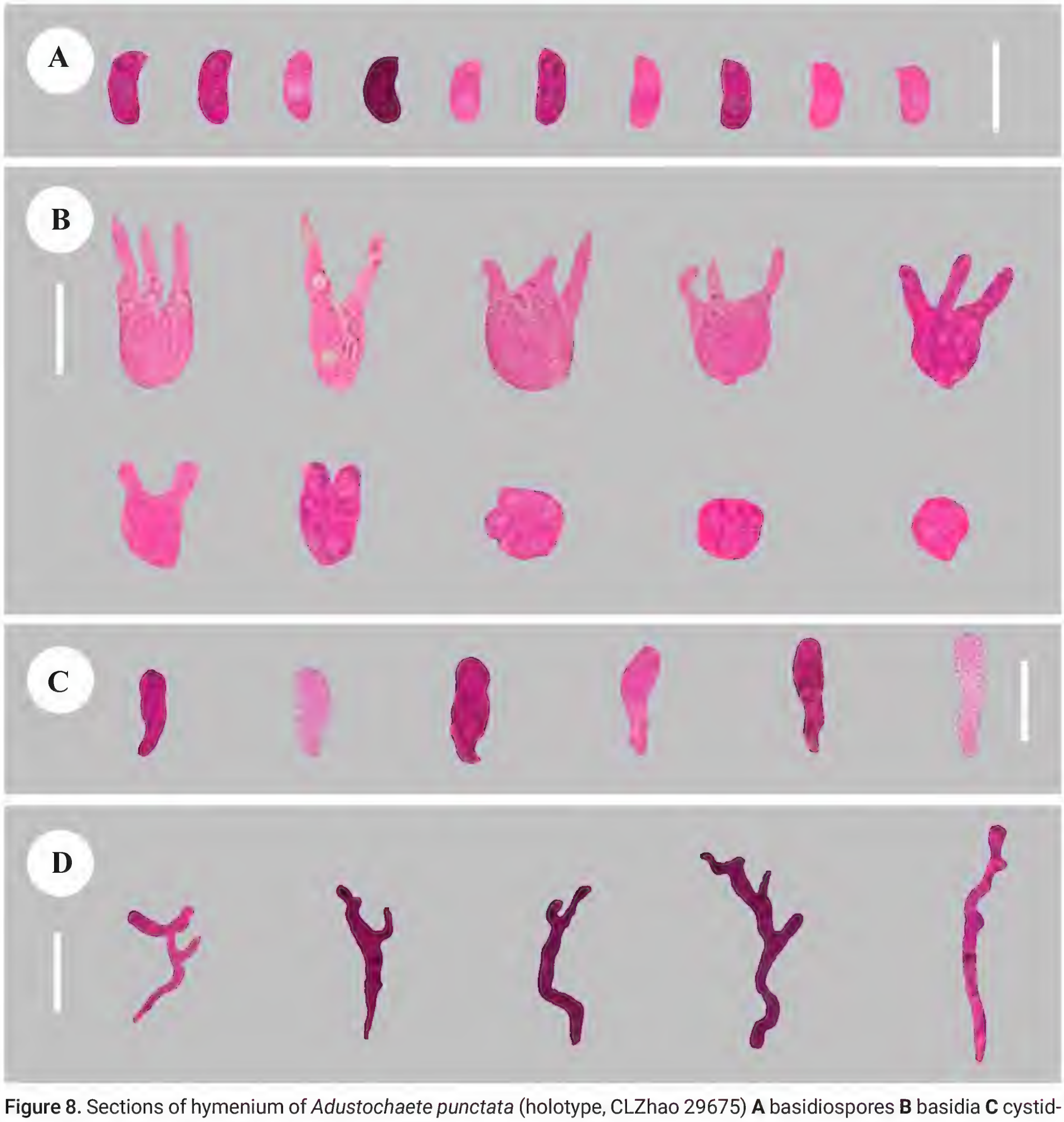

Figure 8. Sections of hymenium of *Adustochaete punctata* (holotype, CLZhao 29675) **A** basidiospores **B** basidia **C** cystidia **D** hyphidia. Scale bars: 20 μm (**A–D**); 10 × 100 Oil.

Basidiomata. Annual, resupinate, closely adnate, membranaceous, very hard to separate from substrate, without odour or taste when fresh, becoming coriaceous upon drying, up to 10 cm long, 1.5 cm wide, 100–250 μm thick. Hymenial surface smooth, punctate, white to cream when fresh, turning to cream upon drying. Sterile margin cream, thinning out, up to 1 mm wide.

Hyphal system. Monomitic, generative hyphae with clamp connections, colourless, thin-walled, unbranched, interwoven, 1.5–3.5 μm in diameter; IKI–, CB–, tissues unchanged in KOH. ***Hymenium.*** Cystidia numerous, thin-walled, subcylindrical to clavate with an obtuse apex, occasionally sinuous in the basal, 15.5–23.5 × 5.5–7.5 μm, with a clamp connection at base; cystidioles absent. Hyphidia arising from generative hyphae, nodulose, branched, colourless, thin-

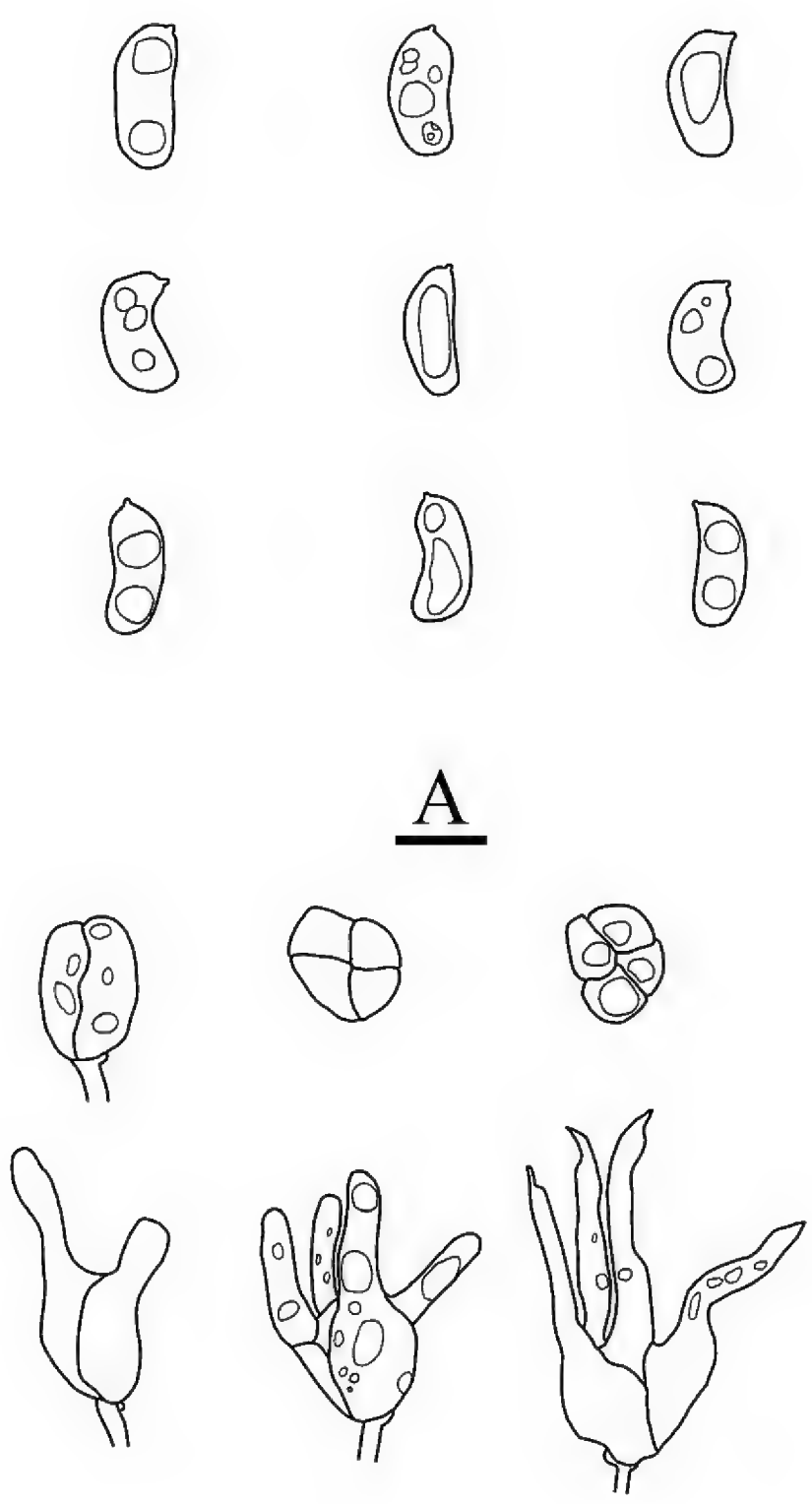

Figure 9. Microscopic structures of *Adustochaete punctata* (holotype, CLZhao 29675) **A** basidiospores **B** basidia **C** basidioles **D** cystidia **E** hyphidia **F** part of the vertical section of hymenium. Scale bars: 10 μm (**A–F**).

walled, 1.5–5 μm in diameter. Basidia ellipsoid to ovoid, longitudinally septate, two to four-celled, 17–25 × 16.5–21 μm; basidioles dominant, similar to basidia in shape, but slightly smaller. ***Basidiospores.*** Subcylindrical to allantoid, slightly curved, colourless, smooth, thin-walled, with several oil drops, IKI–, CB–, (13–)13.5–18(–18.5) × (5.5–)6–8.2(–8.5) μm, L = 15.78 μm, W = 6.79 μm, Q = 2.15–2.40 Q_m = 2.32 ± 0.08 (n = 90/3).

Additional specimens examined. CHINA • Yunnan Province, Dehong, Yingjiang County, Tongbiguan Provincial Nature Reserve, 23°48'N, 97°38'E, altitude 1500 m, on the fallen branch of angiosperm, leg. C.L. Zhao, 17 July 2023, CLZhao 29669; CLZhao 29671; CLZhao 29685; CLZhao 29686; CLZhao 29706; CLZhao 29710; CLZhao 29711 (SWFC).

***Alloexidiopsis grandinea* J.H Dong & C.L. Zhao, sp. nov.**

MycoBank No: 854171

Figs 10–12

Diagnosis. Differs from other *Alloexidiopsis* species by its membranaceous basidiomata with buff to slightly yellowish, grandinioid hymenial surface, a monomitic hyphal system with clamped generative hyphae and cylindrical to allantoid basidiospores measuring 10–12.3 × 5–5.8 µm.

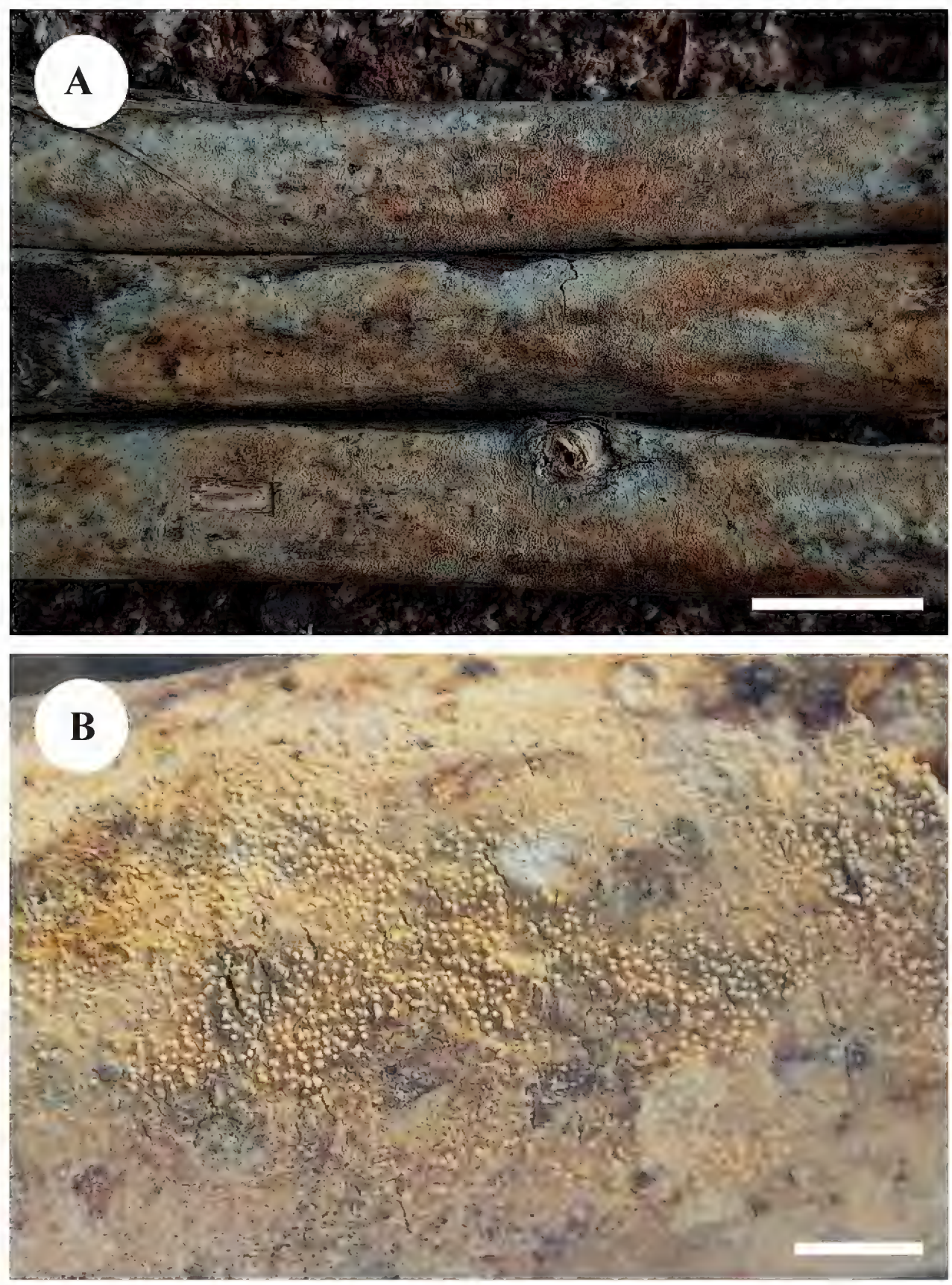

Figure 10. Basidiomata of *Alloexidiopsis grandinea* in general and detailed views (CLZhao 33798, holotype). Scale bars: 1 cm (**A**); 1 mm (**B**).

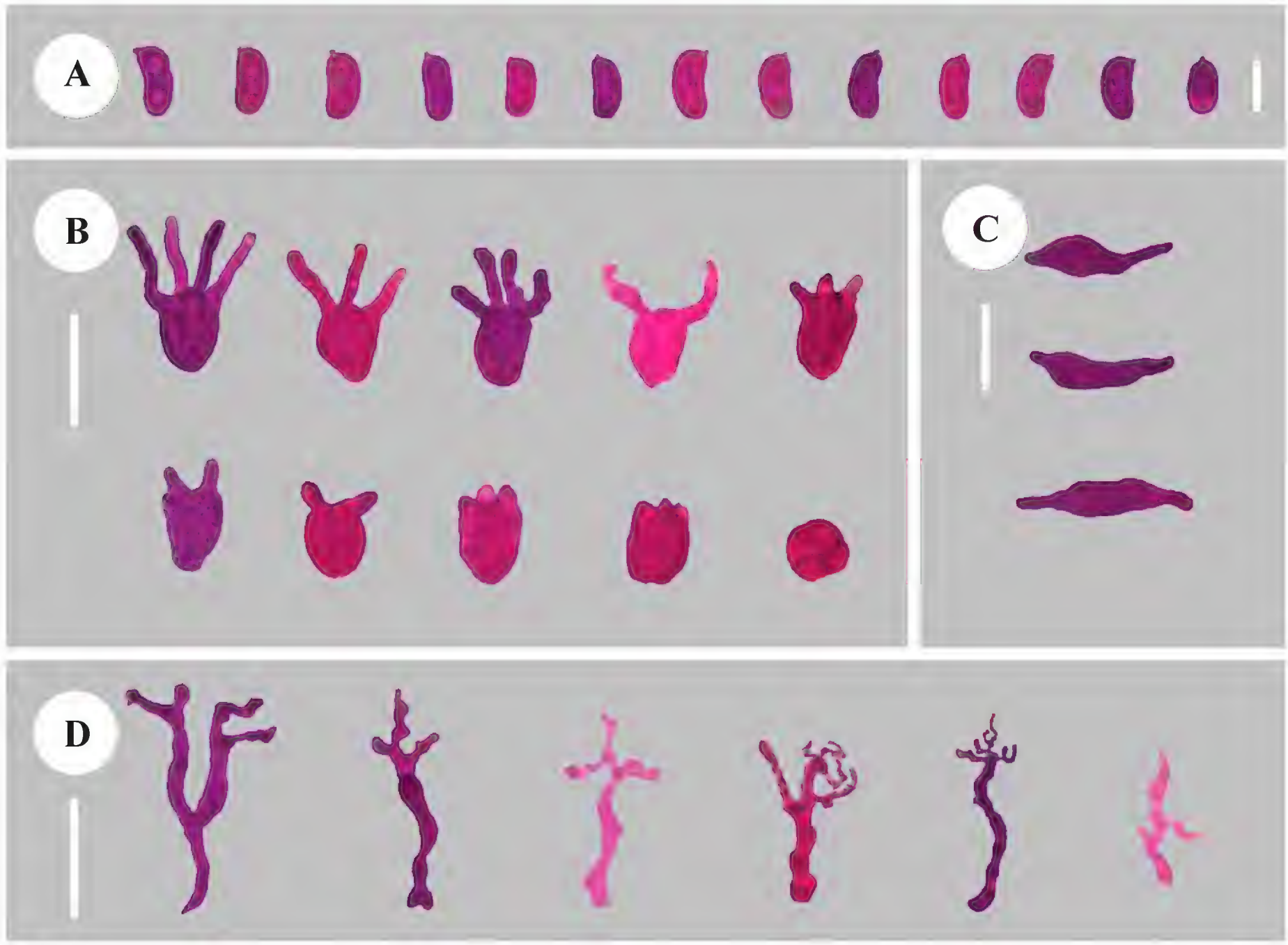

Figure 11. Sections of hymenium of *Alloexidiopsis grandinea* (holotype, CLZhao 33798) **A** basidiospores **B** basidia **C** cystidia **D** hyphidia. Scale bars: 10 μm (**A**); 20 μm (**B–D**); 10 × 100 Oil.

Holotype. China • Yunnan Province, Zhaotong, Wumengshan National Nature Reserve, 28°03'N, 104°20'E, altitude 1500 m, on the fallen branch of angiosperm, leg. C.L. Zhao, 21 September 2023, CLZhao 33798 (SWFC).

Etymology. *grandinea* (Latin or Greek origin): referring to the grandinioid hymenial surface.

Basidiomata. Annual, resupinate, closely adnate, membranaceous, very hard to separate from substrate, without odour or taste when fresh, becoming coriaceous upon drying, up to 20 cm long, 3 cm wide, 50–100 μm thick. Hymenial surface grandinioid, white to buff when fresh, turning to buff to slightly yellowish upon drying. Sterile margin cream to buff, thinning out, up to 1 mm wide.

Hyphal system. Monomitic, generative hyphae with clamp connections, colourless, thin-walled, rarely branched, interwoven, 2–4 μm in diameter; IKI–, CB–, tissues unchanged in KOH. ***Hymenium.*** Cystidia numerous, thin-walled, fusiform with an acute apex, occasionally sinuous in the basal, 20–42.5 × 5.5–9.5 μm, with a clamp connection at base; cystidioles absent. Hyphidia arising from generative hyphae, nodulose, frequently branched, colourless, thin-walled, 2–5 μm in diameter. Basidia ellipsoid to ovoid, longitudinally septate, two to four-celled, 12.5–14.5 × 9–11.5 μm; basidioles dominant, similar to basidia in shape, but slightly smaller. ***Basidiospores.*** Cylindrical to allantoid, slightly curved, colourless, smooth, thin-walled, with 1–2 oil drops, IKI–, CB–, (9.5–)10–12.3(–12.5) × (4.8–)5–5.8(–6) μm, L = 11.08 μm, W = 5.38 μm, Q = 1.95–2.20, Q_m = 2.06 ± 0.04 (n = 60/2).

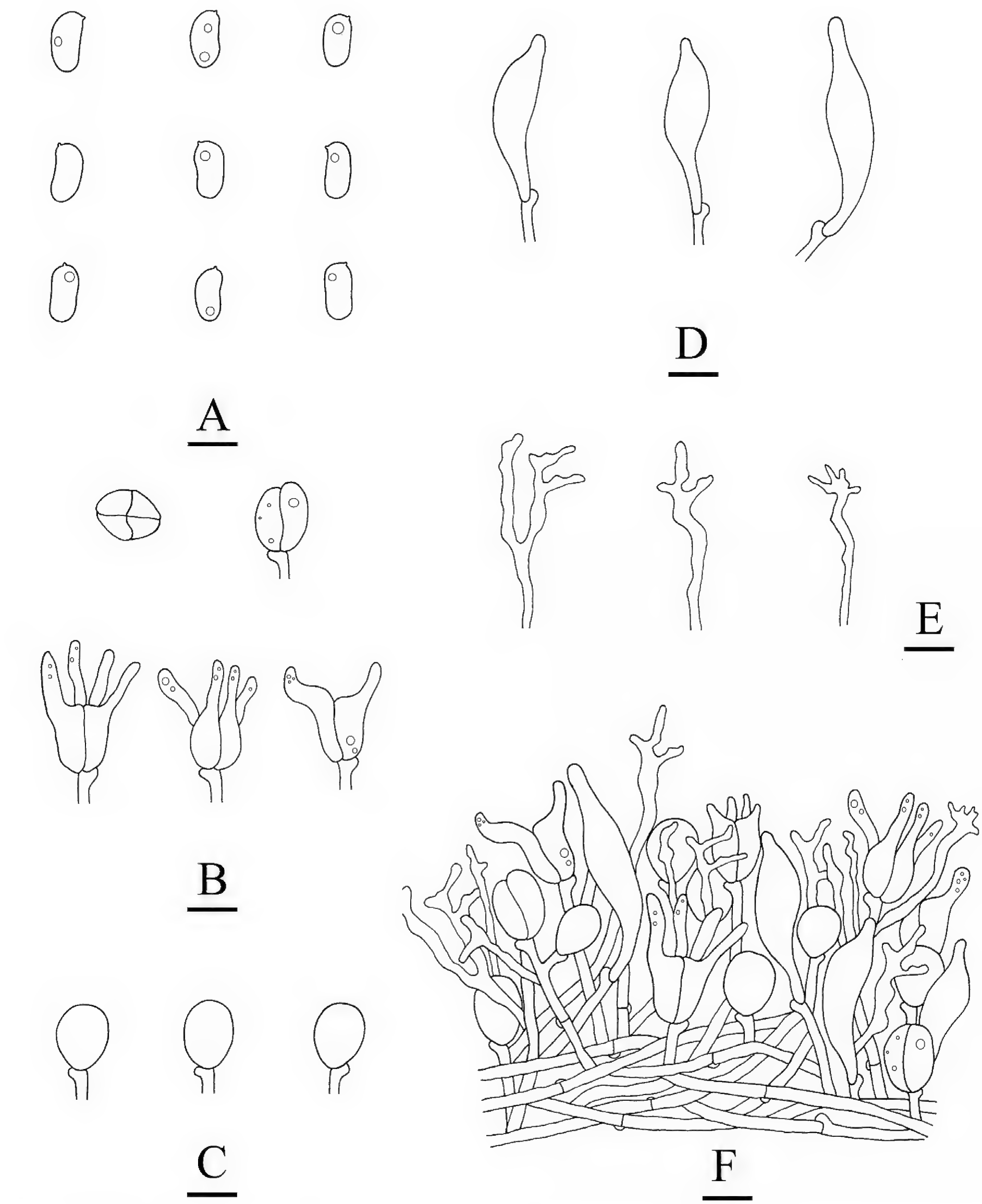

Figure 12. Microscopic structures of *Alloexidiopsis grandinea* (holotype, CLZhao 33798) **A** basidiospores **B** basidia **C** basidioles **D** cystidia **E** hyphidia **F** part of the vertical section of hymenium. Scale bars: 10 μm (**A–F**).

Additional specimen examined. China • Yunnan Province, Diqing, Weixi County, Weiden Town, Fuchuan Village, 27°06'N, 99°10'E, altitude 2900 m, on the fallen branch of angiosperm, leg. C.L. Zhao, 12 October 2023, CLZhao 34279 (SWFC).

Alloexidiopsis xantha **J.H. Dong & C.L. Zhao, sp. nov.**

MycoBank No: 854172

Figs 13–15

Diagnosis. Differs from other *Alloexidiopsis* species by its coriaceous basidiomata with cream to buff to yellow, smooth, slightly cracked hymenial surface, a monomitic hyphal system with clamped generative hyphae and allantoid to sickle-shaped basidiospores measuring 20–24 × 5–6.2 µm.

Holotype. CHINA • Yunnan Province, Lincang, Yun County, Dumu Village, 24°32'N, 100°23'E, altitude 2100 m, on the fallen branch of angiosperm, leg. C.L. Zhao, 20 October 2022, CLZhao 25093 (SWFC).

Etymology. *xantha* (Latin or Greek origin): referring to the buff to yellow hymenial surface of the type specimen.

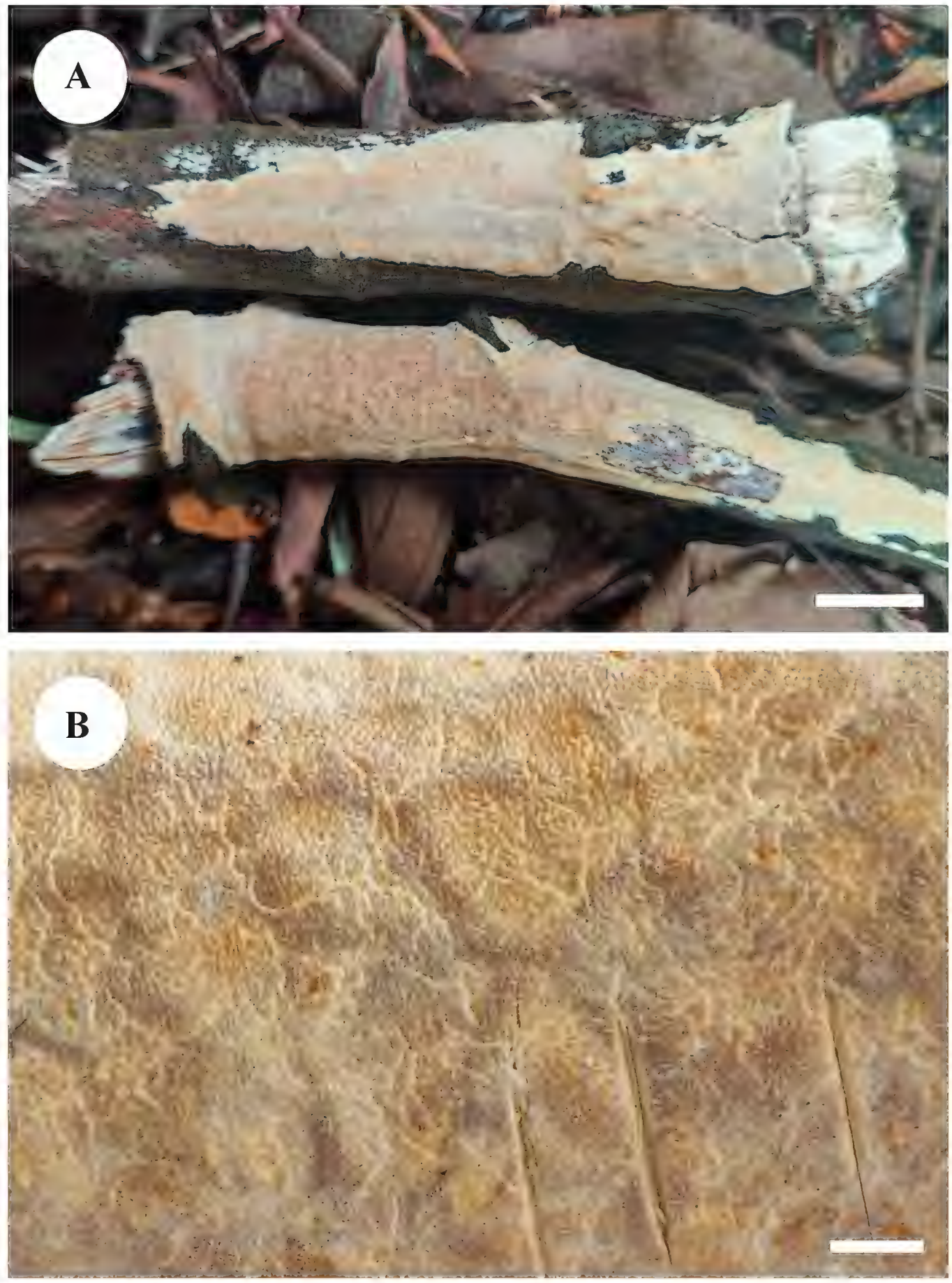

Figure 13. Basidiomata of *Alloexidiopsis xantha* in general and detailed views (CLZhao 25093, holotype). Scale bars: 1 cm (**A**); 1 mm (**B**).

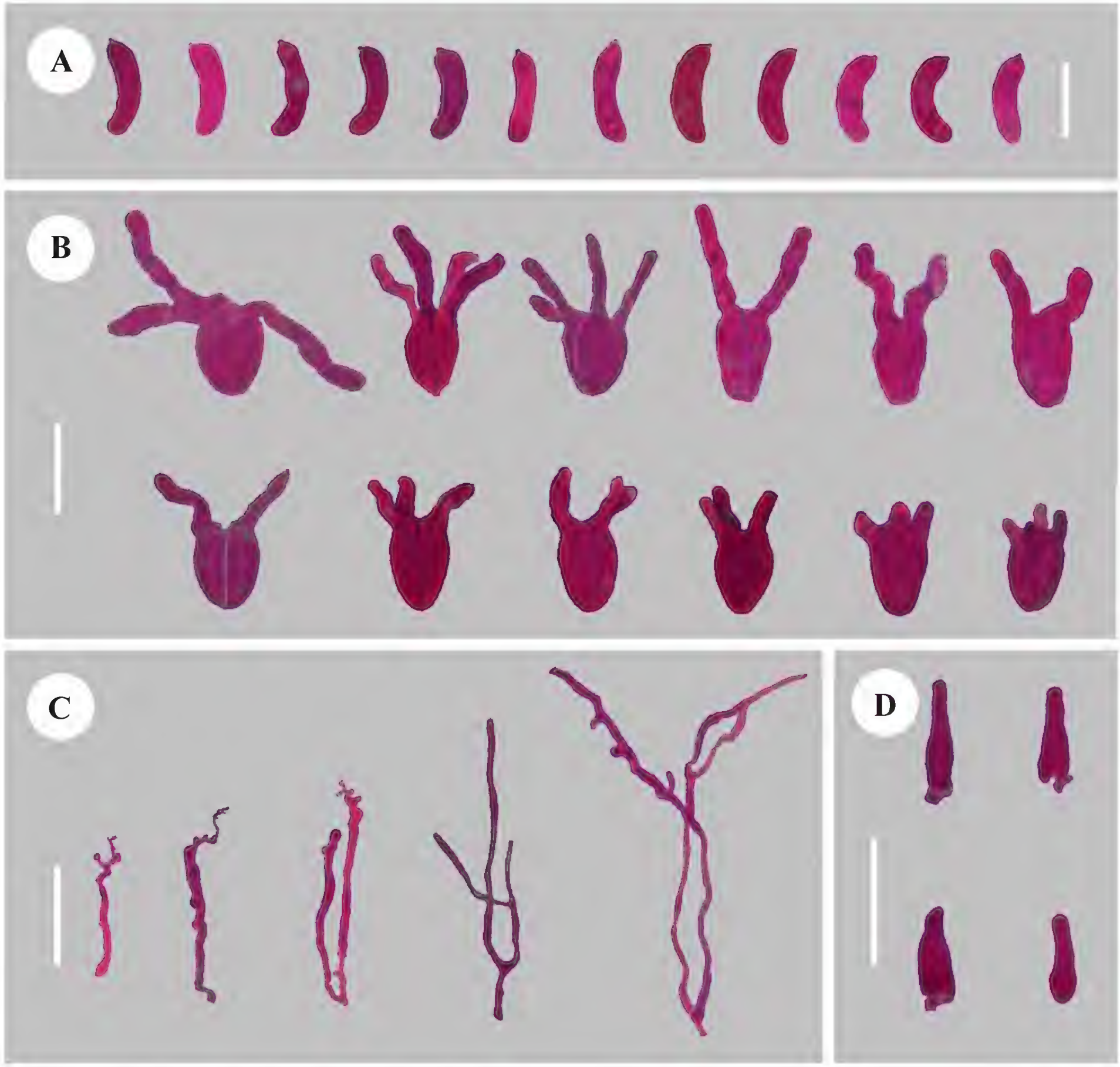

Figure 14. Sections of hymenium of *Alloexidiopsis xantha* (holotype, CLZhao 25093) **A** basidiospores **B** basidia **C** hyphidia **D** cystidia. Scale bars: 20 μm (**A–D**); 10 × 100 Oil.

Basidiomata. Annual, resupinate, closely adnate, coriaceous, very hard to separate from substrate, without odour or taste when fresh, becoming leathery upon drying, up to 10 cm long, 2 cm wide, 200–300 μm thick. Hymenial surface smooth, slightly cracked, cream when fresh, turning to cream to buff to yellow upon drying. Sterile margin cream, thinning out, up to 1 mm wide.

Hyphal system. Monomitic, generative hyphae with clamp connections, colourless, thin- to thick walled, branched, interwoven, 2.5–3.5 μm in diameter; IKI–, CB–, tissues unchanged in KOH. ***Hymenium.*** Cystidia numerous, thin-walled, subcylindrical to subconiform with an obtuse apex, 12.5–17.5 × 3.5–6 μm, with a clamp connection at base; cystidioles absent. Hyphidia arising from generative hyphae, nodulose, frequently branched, colourless, thin-walled, 2.5–4 μm in diameter. Basidia ellipsoid to ovoid, obconical, longitudinally septate, two to four-celled, 18–20.5 × 12–15.5 μm; basidioles dominant, similar to basidia in

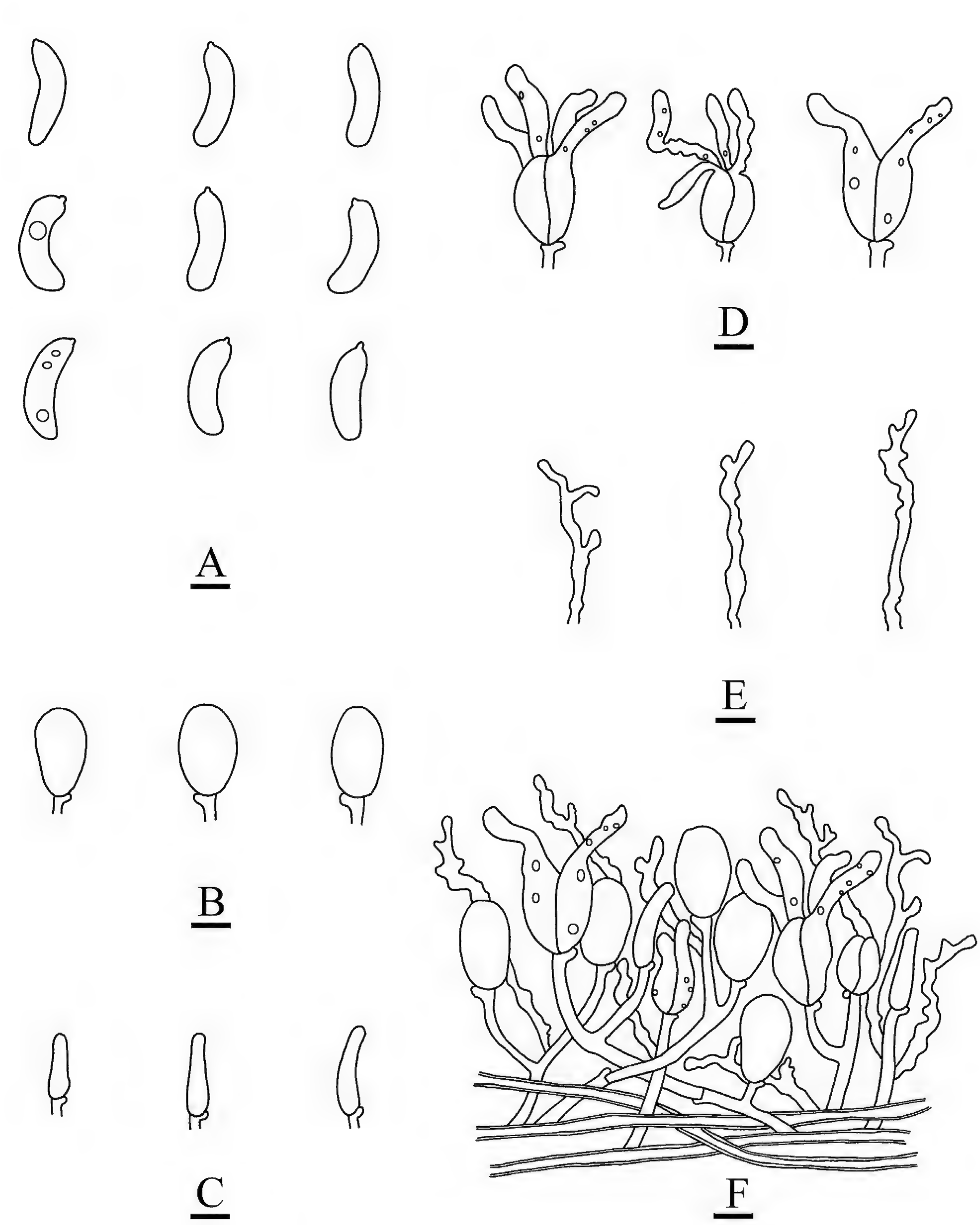

Figure 15. Microscopic structures of *Alloexidiopsis xantha* (holotype, CLZhao 25093) **A** basidiospores **B** basidioles **C** cystidia **D** basidia **E** hyphidia **F** part of the vertical section of hymenium. Scale bars: 10 μm (**A–F**).

shape, but slightly smaller. ***Basidiospores.*** Allantoid, curved, sickle-shaped, colourless, smooth, thin-walled, IKI–, CB–, (18.5–)20–24(–24.5) × 5–6.2(–6.5) μm, L = 21.66 μm, W = 5.63 μm, Q = 3.60–4.05, Q_m = 3.85 ± 0.10 (n = 30/1).

Discussion

In the present study, four new species *Ad. albomarginata*, *Ad. punctata*, *Al. grandinea* and *Al. xantha* are described, based on the phylogenetic analyses and morphological characteristics.

The corticioid species of the order Auriculariales are traditionally placed in *Eichleriella*, *Exidiopsis* and *Heterochaete* according to the morphological characteristics (Liu et al. 2022). On the basis of the erection of six new genera as *Adustochaete*, *Alloexidiopsis*, *Amphistereum*, *Crystallodon*, *Proterochaete* and *Sclerotrema*, they were placed in the corticioid species and three previously known genera were reinstated, for example, *Hirneolina*, *Heteroradulum* and *Tremellochaete* (Malysheva and Spirin 2017; Alvarenga et al. 2019; Alvarenga and Gibertoni 2021; Liu et al. 2022). A multilocus-based phylogeny with a wider sampling of various morphological groups in Auriculariales is urgently needed to achieve a more natural classification of this order, as in other orders within Agaricomycetes (Wang et al. 2021).

Phylogenetically, based on the combined ITS+nLSU sequence data (Fig. 1), it demonstrated that the four new species were nested in the genera *Adustochaete* and *Alloexidiopsis* within the order Auriculariales. Based on ITS topology tree (Fig. 2), *Ad. albomarginata* was retrieved as a sister to *Ad. yunnanensis* and the species *Ad. punctata* was sister to *Ad. rava*. However, *Ad. yunnanensis* differs from *Ad. albomarginata* by its grandinioid hymenial surface, longer basidia (25–47.5 × 8.5–14 µm) and smaller cystidia (17.5–24.5 × 3.5–5.8 µm; Li and Zhao (2022)). *Ad. rava* can be distinguished from *Ad. punctata* by its spined, sharp-tipped hymenial surface, smaller basidia (14.9–16.2 × 9.7–10.1 µm) and basidiospores (10.2–13.6 × 4.6–5.9 µm; Hyde et al. (2020)). Based on ITS topology tree (Fig. 3),

Table 2. A morphological comparison between two new *Adustochaete* species and four similar species in the genus *Adustochaete*.

Species name	Hymenial surface	Hyphae	Cystidia	Basidia	Basidiospores	References
Adustochaete albomarginata	Smooth/ Cream to buff	Thin-walled, unbranched	Subclavate to fusiform; 23.5–48.5 × 10–13.5 µm	Ellipsoid to ovoid, two to four-celled; 17–24.5 × 11–16.5 µm	Subcylindrical to allantoid; 12–17.5 × 6.5–9 µm	**Present study**
Adustochaete interrupta	Smooth/ Light ochraceous-grey to brownish	Thin-walled	Clavate to fusiform; 45–96 × 6–13.5 µm	Narrowly ovoid to obconical, four-celled; 15.1–24 × 9.1–11.8 µm	Broadly cylindrical; 11.3–14.3 × 5.7–6.2 µm	Alvarenga et al. (2019)
Adustochaete nivea	Sharp-tipped spines/ White	Thin-walled	—	Narrowly ovoid to obconical, four-celled; 14.9–16.2 × 9.7–10.1 µm	Cylindrical; 10.2–13.6 × 4.6–5.9 µm	Hyde et al. (2020)
Adustochaete punctata	Smooth/ Punctate, white to cream	Thin-walled, unbranched	Subcylindrical to clavate; 15.5–23.5 × 5.5–7.5 µm	Ellipsoid to ovoid, two to four-celled; 17–25 × 16.5–21 µm	Subcylindrical to allantoid; 13.5–18 × 6–8.2 µm	**Present study**
Adustochaete rava	Sharp-tipped spines/ Pale to dark grey	Thin-walled	Clavate to fusiform; 27–52 × 4–8 µm	Narrowly ovoid to obconical, four-celled; 10.8–15.2 × 7.3–10 µm	Cylindrical; 10.2–13.7 × 3.8–4.7 µm	Alvarenga et al. (2019)
Adustochaete yunnanensis	Grandinioid/ Dark greyish to brownish	Thin-walled, branched	Clavate to fusiform; 17.5–24.5 × 3.5–5.8 µm	Narrowly ovoid to obconical, four-celled; 25–47.5 × 8.5–14 µm	Narrow cylindrical to allantoid; 12–20 × 5–7 µm	Li and Zhao (2022)

Al. grandinea was retrieved as a sister to *Al. schistacea* and *Al. xantha* formed a monophyletic lineage. However, *Al. schistacea* differs from *Al. grandinea* by its smooth hymenial surface and longer basidia (15–20 × 7–10 µm; Liu et al. (2022)).

Morphologically, two new species *Adustochaete albomarginata* and *Ad. punctata* resemble four similar species in the genus *Adustochaete*, *Ad. interrupta* Spirin & Malysheva, *Ad. nivea*, *Ad. rava* and *Ad. yunnanensis*. A morphological comparison between two new *Adustochaete* species and four similar species are presented in Table 2. Two new species *Al. grandinea* and *Al. xantha* are similar to five species in the genus *Alloexidiopsis*, *Al. australiensis* S.L. Liu, Z.Q. Shen & L.W. Zhou, *Al. calcea* (Pers.) L.W. Zhou & S.L. Liu, *Al. nivea* (J.J. Li & C.L. Zhao) L.W. Zhou & S.L. Liu, *Al. schistacea* and *Al. yunnanensis*. A morphological comparison between two new *Alloexidiopsis* species and six similar species are presented in Table 3.

In the ecological distribution, both genera species are not an extensively studied group, distributed worldwide and mainly found on hardwood (Alvarenga et al. 2019; Liu et al. 2022). The species of *Adustochaete interrupta* Spirin & Malysheva was found in Mexico, *Ad. nivea* was described in Brazil, *Ad. rava* was found in Brazil and *Ad. yunnanensis* was found in China. The species of *Alloexidiopsis australiensis* was found in Australia, *Al. calcea* was found in Germany and *Al. nivea*, *Al. schistacea*, *Al. sinensis* and *Al. yunnanensis* were found in China.

Table 3. A morphological comparison between two new *Alloexidiopsis* species and six similar species in the genus *Alloexidiopsis*.

Species name	Hymenial surface	Hyphae	Cystidia	Basidia	Basidiospores	References
Alloexidiopsis australiensis	Smooth, covered by sterile spines/ Cream to pale orange	Thin-walled, branched	Cylindrical, ventricose; 21.5–24.5 × 9.5–12 µm	Ellipsoid to ovoid, four-celled; 18–21 × 13–18 µm	Cylindrical to broadly cylindrical; 13–25 × 7–11 µm	Li et al. (2022b)
Alloexidiopsis calcea	Granulose to pruinose/ Greyish-white to light ochraceous	Thin-walled, branched	–	Obovate to clavate, two to four-celled; 14–25 × 9.5–15 µm	Allantoid to cylindrical, sometimes helicoid; 12–18 × 5–7 µm	Wells (1961)
Alloexidiopsis grandinea	Grandinioid/ Buff to slightly yellowish	Thin-walled, branched	Fusiform; 20–42.5 × 5.5–9.5 µm	Ellipsoid to ovoid, two to four-celled; 12.5–14.5 × 9–11.5 µm	Cylindrical to allantoid; 10–12.3 × 5–5.8 µm	**Present study**
Alloexidiopsis nivea	Smooth/ White to slightly cream	Thin-walled, unbranched	Tubular; 15–34 × 2.5–7 µm	Narrowly ovoid to obconical, two to four-celled; 9–19 × 8–15 µm	Allantoid; 6.5–13.5 × 2.7–5.5 µm	Li et al. (2022a)
Alloexidiopsis schistacea	Smooth/ Greyish	Thin-walled, branched	Cylindrical; 25–50 × 4–6 µm	Ellipsoid to ovoid, four-celled; 15–20 × 7–10 µm	Cylindrical to broadly cylindrical; 9.5–11 × 4.5–5.5 µm	Liu et al. (2022)
Alloexidiopsis sinensis	Grandinoid/ Yellowish-brown to rose to slightly purple	Thin- to thick-walled, branched	Cylindrical; 11.5–15.5 × 3–5.5 µm	Ellipsoid to ovoid, two to four-celled; 16–22 × 7.5–10 µm	Allantoid; 14.5–23 × 4.5–6.5 µm	Dong et al. (2024)
Alloexidiopsis xantha	Smooth/ Cream to slightly buff	Thin- to thick walled, branched	Subcylindrical to subconiform; 12.5–17.5 × 3.5–6 µm	Ellipsoid to ovoid, obconical; 18–20.5 × 12–15.5 µm	Allantoid, sickle-shaped; 20–24 × 5–6.2 µm	**Present study**
Alloexidiopsis yunnanensis	Odontoid/ White to smoke grey	Thin-walled, unbranched	Clavate to fusiform; 13–35 × 2–6 µm	Narrowly ovoid to obconical, two to three-celled; 28–41 × 9–14 µm	Cylindrical; 17–24 × 5–8 µm	Guan et al. (2020)

Fungi are one of the most diverse groups of organisms on Earth and play a crucial role in ecosystem processes and functions (Hyde 2022). New DNA sequencing techniques have revolutionised the studies of fungal taxonomy and diversity, in which about 150 k species of fungi have been described (Hyde 2022). In recent years, the wood-inhabiting fungi are an extensively studied group of Basidiomycota, which includes a number of poroid, smooth, grandinoid, odontioid and hydnoid basidiomata in China (Wu et al. 2022a, 2022b; Dong et al. 2023a, 2023b; Guan et al. 2023; Liu et al. 2023; Mao et al. 2023; Yang et al. 2023, 2024; Deng et al. 2024; Li et al. 2024; Luo et al. 2024; Zhang et al. 2024; Zhao et al. 2024; Zhou et al. 2024). In the past several years, many corticioid species have been reported and described in the order Auriculariales (Malysheva and Spirin 2017; Alvarenga et al. 2019; Spirin et al. 2019a, 2019a; Alvarenga and Gibertoni 2021; Li et al. 2022a, 2022b; Li and Zhao 2022; Liu et al. 2022), but many new taxa have not yet been discovered. Thus, the corticioid species diversity of the order Auriculariales is still not well known in China, especially in the subtropical and tropical areas. In the present study, four new species, *Ad. albomarginata*, *Ad. punctata*, *Al. grandinea* and *Al. xantha* were found and reported. This paper enriches our knowledge of fungal diversity in the order Auriculariales. We anticipate that more undescribed corticioid taxa will be discovered throughout China after extensive collection combined with morphological and molecular analyses.

Key to the known species of *Adustochaete* worldwide

1 Hymenial surface smooth **2**
– Hymenial surface grandinioid **4**
2 Basidia > 16.5 µm wide ..... ***Adustochaete punctata***
– Basidia < 16.5 µm wide **3**
3 Basidiospores > 6.5 µm wide ..... ***Adustochaete albomarginata***
– Basidiospores < 6.5 µm wide ..... ***Adustochaete interrupta***
4 Cystidia absent ..... ***Adustochaete nivea***
– Cystidia present **5**
5 Basidiospores > 5 µm wide, basidia > 16 µm long ..... ***Adustochaete yunnanensis***
– Basidiospores < 5 µm wide, basidia < 16 µm long ..... ***Adustochaete rava***

Key to the known species of *Alloexidiopsis* worldwide

1 Basidiospores allantoid **2**
– Basidiospores cylindrical **6**
2 Hymenial surface smooth **3**
– Hymenial surface grandinoid, granulose to pruinose **4**
3 Basidiospores > 13.5 µm long, cystidia subcylindrical to subconiform ..... ***Alloexidiopsis xantha***
– Basidiospores < 13.5 µm long, cystidia tubular ..... ***Alloexidiopsis nivea***
4 Cystidia absent ..... ***Alloexidiopsis calcea***
– Cystidia present **5**
5 Cystidia > 5.5 µm wide ..... ***Alloexidiopsis grandinea***
– Cystidia < 5.5 µm wide ..... ***Alloexidiopsis sinensis***

6 Basidia > 28 µm long, cystidia clavate to fusiform ..... ***Alloexidiopsis yunnanensis***

– Basidia < 28 µm long, cystidia cylindrical **7**

7 Basidiospores > 11 µm long, cystidia < 25 µm long ..... ***Alloexidiopsis australiensis***

– Basidiospores < 11 µm long, cystidia > 25 µm long ..... ***Alloexidiopsis schistacea***

Additional information

Conflict of interest

The authors have declared that no competing interests exist.

Ethical statement

No ethical statement was reported.

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Author contributions

Conceptualisation, CZ and JD; methodology, CZ and JD; software, CZ, JD and YZ; validation, CZ and JD; formal analysis, CZ and J JD; investigation, CZ and JD; resources CZ; writing – original draft preparation, CZ, JD, YZ and CQ; writing – review and editing, CZ and JD; visualisation, CZ and JD; supervision, CZ and JD; project administration, CZ; funding acquisition, CZ. All authors have read and agreed to the published version of the manuscript.

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Data availability

All of the data that support the findings of this study are available in the main text.

References

Alvarenga RLM, Gibertoni TB (2021) *Crystallodon* Alvarenga gen. nov., a new genus of the Auriculariales from the Neotropics. Cryptogamie. Mycologie 42(2): 17–24. https://doi.org/10.5252/cryptogamie-mycologie2021v42a2

Alvarenga RLM, Spirin V, Malysheva V, Gibertoni TB, Larsson KH (2019) Two new genera and six other novelties in *Heterochaete* sensu lato (Auriculariales, Basidiomycota). Botany 97(8): 439–451. https://doi.org/10.1139/cjb-2019-0046

Chen YL, Su MS, Zhang LP, Zou Q, Wu F, Zeng NK, Liu M (2020) *Pseudohydnum brunneiceps* (Auriculariales, Basidiomycota), a new species from Central China. Phytotaxa 441: 87–94. https://doi.org/10.11646/phytotaxa.441.1.8

Darriba D, Taboada GL, Doallo R, Posada D (2012) jModelTest 2: More models, new heuristics and parallel computing. Nature Methods 9(8): 772. https://doi.org/10.1038/nmeth.2109

Deng Y, Jabeen S, Zhao C (2024) Species diversity and taxonomy of *Vararia* (Russulales, Basidiomycota) with descriptions of six species from Southwestern China. MycoKeys 103: 97–128. https://doi.org/10.3897/mycokeys.103.118980

Dong JH, Gu JY, Zhao CL (2023a) Diversity of wood-decaying fungi in Wenshan Area, Yunnan Province, China. Junwu Xuebao 42: 638–662. https://doi.org/10.13346/j.mycosystema.220205

Dong JH, Zhang XC, Chen JJ, Zhu ZL, Zhao CL (2023b) A phylogenetic and taxonomic study on *Steccherinum* (Polyporales, Basidiomycota): Focusing on three new *Steccherinum* species from Southern China. Frontiers in Cellular and Infection Microbiology 12: 1103579. https://doi.org/10.3389/fcimb.2022.1103579

Dong JH, Gu ZR, Wang YY, Shi YM, Zhao CL (2024) A new corticioid fungus, *Alloexidiopsis sinensis* (Auriculariales, Basidiomycota), in China, evidenced by morphological characteristics and phylogenetic analyses. Phytotaxa 658(3): 227–239. https://doi.org/10.11646/phytotaxa.658.3.1

Felsenstein J (1985) Confidence intervals on phylogenetics: An approach using bootstrap. Evolution; International Journal of Organic Evolution 39(4): 783–791. https://doi.org/10.2307/2408678

Guan QX, Liu CM, Zhao TJ, Zhao CL (2020) *Heteroradulum yunnanensis* sp. nov. (Auriculariales, Basidiomycota) evidenced by morphological characters and phylogenetic analyses in China. Phytotaxa 437(2): 51–59. https://doi.org/10.11646/phytotaxa.437.2.1

Guan QX, Huang J, Huang J, Zhao CL (2023) Five new species of Schizoporaceae (Basidiomycota, Hymenochaetales) from East Asia. MycoKeys 96: 25–56. https://doi.org/10.3897/mycokeys.96.99327

Hibbett DS, Binder M, Bischoff JF, Blackwell M, Cannon PF, Eriksson OE, Huhndorf S, James T, Kirk PM, Lücking R, Thorsten Lumbsch H, Lutzoni F, Matheny PB, McLaughlin DJ, Powell MJ, Redhead S, Schoch CL, Spatafora JW, Stalpers JA, Vilgalys R, Aime MC, Aptroot A, Bauer R, Begerow D, Benny GL, Castlebury LA, Crous PW, Dai YC, Gams W, Geiser DM, Griffith GW, Gueidan C, Hawksworth DL, Hestmark G, Hosaka K, Humber RA, Hyde KD, Ironside JE, Kõljalg U, Kurtzman CP, Larsson KH, Lichtwardt R, Longcore J, Miadlikowska J, Miller A, Moncalvo JM, Mozley-Standridge S, Oberwinkler F, Parmasto E, Reeb V, Rogers JD, Roux C, Ryvarden L, Sampaio JP, Schüssler A, Sugiyama J, Thorn RG, Tibell L, Untereiner WA, Walker C, Wang Z, Weir A, Weiss M, White MM, Winka K, Yao YJ, Zhang N (2007) A higher-level phylogenetic classification of the Fungi. Mycological Research 111(5): 509–547. https://doi.org/10.1016/j.mycres.2007.03.004

Hibbett DS, Bauer R, Binder M, Giachini AJ, Hosaka K, Justo A, Larsson E, Larsson KH, Lawrey JD, Miettinen O, Nagy LG, Nilsson RH, Weiss M, Thorn RG (2014) 14 Agaricomycetes. In: McLaughlin D, Spatafora J (Eds) Systematics and Evolution. The Mycota, vol 7A. Springer, Berlin, Heidelberg, 373–430. https://doi.org/10.1007/978-3-642-55318-9_14

Hyde KD (2022) The numbers of fungi. Fungal Diversity 114(1): 1. https://doi.org/10.1007/s13225-022-00507-y

Hyde KD, Dong Y, Phookamsak R, Jeewon R, Bhat DJ, Jones EBG, Liu NG, Abeywickrama PD, Mapook A, Wei DP, Perera RH, Manawasinghe IS, Pem D, Bundhun D, Karunarathna A, Ekanayaka AH, Bao DF, Li JF, Samarakoon MC, Chaiwan N, Lin CG, Phutthacharoen K, Zhang SN, Senanayake IC, Goonasekara ID, Thambugala KM, Phukhamsakda C, Tennakoon DS, Jiang HB, Yang J, Zeng M, Huanraluek N, Liu JK, Wijesinghe SN, Tian Q, Tibpromma S, Brahmanage RS, Boonmee S, Huang SK, Thiyagaraja V, Lu YZ, Jayawardena RS, Dong W, Yang EF, Singh SK, Singh SM, Rana S, Lad SS, Anand G, Devadatha B, Niranjan M, Sarma VV, Liimatainen K, Aguirre-Hudson B, Niskanen T, Overall A, Alvarenga RLM, Gibertoni TB, Pfliegler WP, Horváth E, Imre A, Alves AL, Santos ACS, Tiago PV, Bulgakov TS, Wanasinghe DN, Bahkali AH, Doilom M, Elgorban AM, Maharachchikumbura SSN, Rajeshkumar KC, Haelewaters D, Mortimer PE, Zhao Q, Lumyong S, Xu JC, Sheng J (2020) Fungal diversity notes 1151–1276: Taxonomic and phylogenetic contributions on genera and species of fungal taxa. Fungal Diversity 100(1): 5–277. https://doi.org/10.1007/s13225-020-00439-5

James TY, Stajich JE, Hittinger CT, Rokas A (2020) Toward a fully resolved fungal tree of life. Annual Review of Microbiology 74(1): 291–313. https://doi.org/10.1146/annurev-micro-022020-051835

Katoh K, Rozewicki J, Yamada KD (2019) MAFFT online service: Multiple sequence alignment, interactive sequence choice and visualization. Briefings in Bioinformatics 20(4): 1160–1166. https://doi.org/10.1093/bib/bbx108

Larsson A (2014) AliView: A fast and lightweight alignment viewer and editor for large data sets. Bioinformatics (Oxford, England) 30(22): 3276–3278. https://doi.org/10.1093/bioinformatics/btu531

Li YF, Zhao CL (2022) *Adustochaete yunnanensis* sp. nov. from China. Mycotaxon 137(2): 261–270. https://doi.org/10.5248/137.261

Li JJ, Zhao CL, Liu CM (2022a) The morphological characteristics and phylogenetic analyses revealed an additional taxon in *Heteroradulum* (Auriculariales). Diversity 14(1): 40. https://doi.org/10.3390/d14010040

Li QZ, Liu SL, Wang XW, May TW, Zhou LW (2022b) Redelimitation of *Heteroradulum* (Auriculariales, Basidiomycota) with *H. australiense* sp. nov. MycoKeys 86: 87–101. https://doi.org/10.3897/mycokeys.86.76425

Li Q, Luo YX, Zhao CL (2024) Molecular systematics and taxonomy reveal three new wood-inhabiting fungal species (Basidiomycota) from Yunnan Province, southern China. Mycological Progress 23(1): 30. https://doi.org/10.1007/s11557-024-01968-y

Liu SL, Shen ZQ, Li QZ, Liu XY, Zhou LW (2022) *Alloexidiopsis* gen. nov., a revision of generic delimitation in Auriculariales (Basidiomycota). Frontiers in Microbiology 13: 894641. https://doi.org/10.3389/fmicb.2022.894641

Liu S, Shen LL, Xu TM, Song CG, Gao N, Wu DM, Sun YF, Cui BK (2023) Global diversity, molecular phylogeny and divergence times of the brown-rot fungi within the Polyporales. Mycosphere: Journal of Fungal Biology 14(1): 1564–1664. https://doi.org/10.5943/mycosphere/14/1/18

Luo KY, Su JQ, Zhao CL (2024) Morphological and molecular identification for four new wood-inhabiting species of *Trechispora* (Basidiomycota) from China. MycoKeys 105: 155–178. https://doi.org/10.3897/mycokeys.105.120438

Lutzoni F, Kauff F, Cox CJ, McLaughlin D, Celio G, Dentinger B, Padamsee M, Hibbett D, James TY, Baloch E, Grube M, Reeb V, Hofstetter V, Schoch C, Arnold AE, Miadlikowska J, Spatafora J, Johnson D, Hambleton S, Crockett M, Shoemaker R, Sung GH, Lücking R, Lumbsch T, O'Donnell K, Binder M, Diederich P, Ertz D, Gueidan C, Hansen K, Harris RC, Hosaka K, Lim YW, Matheny B, Nishida H, Pfister D, Rogers J, Rossman

A, Schmitt I, Sipman H, Stone J, Sugiyama J, Yahr R, Vilgalys R (2004) Assembling the fungal tree of life: Progress, classification, and evolution of subcellular traits. American Journal of Botany 91(10): 1446–1480. https://doi.org/10.3732/ajb.91.10.1446

Malysheva V, Spirin V (2017) Taxonomy and phylogeny of the Auriculariales (Agaricomycetes, Basidiomycota) with stereoid basidiocarps. Fungal Biology 121(8): 689–715. https://doi.org/10.1016/j.funbio.2017.05.001

Malysheva V, Spirin V, Miettinen O, Motato-Vásquez V, Hernawati JSSS, Larsson KH (2018) Revision of *Protohydnum* (Auriculariales, Basidiomycota). Mycological Progress 17(7): 805–814. https://doi.org/10.1007/s11557-018-1393-6

Mao WL, Wu YD, Liu HG, Yuan Y, Dai YC (2023) A contribution to *Porogramme* (Polyporaceae, Agaricomycetes) and related genera. IMA Fungus 14(1): 5. https://doi.org/10.1186/s43008-023-00110-z

Miettinen O, Spirin V, Niemelä T (2012) Notes on the genus *Aporpium* (Auriculariales, Basidiomycota), with a new species from temperate Europe. Annales Botanici Fennici 49(5–6): 359–368. https://doi.org/10.5735/085.049.0607

Miller MA, Pfeiffer W, Schwartz T (2012) The CIPRES science gateway. In: Miller MA, Pfeiffer W, Schwartz T(Eds) Proceedings of the 1st Conference of the Extreme Science and Engineering Discovery Environment: Bridging from the Extreme to the Campus and Beyond, Chicago, IL, 39 pp. https://doi.org/10.1145/2335755.2335836

Petersen JH (1996) Farvekort. In: Petersen JH (Ed.) The Danish Mycological Society's Colour-Chart, Foreningen til Svampekundskabens Fremme: Greve, Germany, 6 pp.

Rehner SA, Samuels GJ (1994) Taxonomy and phylogeny of *Gliocladium* analysed from nuclear large subunit ribosomal DNA sequences. Mycological Research 98(6): 625–634. https://doi.org/10.1016/S0953-7562(09)80409-7

Ronquist F, Teslenko M, van der Mark P, Ayres DL, Darling A, Hohna S, Larget B, Liu L, Suchard MA, Huelsenbeck JP (2012) Mrbayes 3.2: Efficient bayesian phylogenetic inference and model choice across a large model space. Systematic Biology 61(3): 539–542. https://doi.org/10.1093/sysbio/sys029

Shen Y, Fan L (2020) Morphological and molecular analyses reveal two new species of *Guepinia* from China. Phytotaxa 475(2): 91–101. https://doi.org/10.11646/phytotaxa.475.2.3

Sotome K, Maekawa N, Nakagiri A, Lee SS, Hattori T (2014) Taxonomic study of Asian species of poroid Auriculariales. Mycological Progress 13(4): 987–997. https://doi.org/10.1007/s11557-014-0984-0

Spirin V, Malysheva V, Larsson KH (2018) On some forgotten species of *Exidia* and *Myxarium* (Auriculariales, Basidiomycota). Nordic Journal of Botany 2018(3): e01601. https://doi.org/10.1111/njb.01601

Spirin V, Malysheva V, Miettinen O, Vlasák J, Alvarenga RLM, Gibertoni TB, Ryvarden L, Larsson KH (2019a) On *Protomerulius* and *Heterochaetella* (Auriculariales, Basidiomycota). Mycological Progress 18(9): 1079–1099. https://doi.org/10.1007/s11557-019-01507-0

Spirin V, Malysheva V, Roberts P, Trichies G, Savchenko A, Larsson KH (2019b) A convolute diversity of the Auriculariales (Agaricomycetes, Basidiomycota) with sphaeropedunculate basidia. Nordic Journal of Botany 2019(7): e02394. https://doi.org/10.1111/njb.02394

Swofford DL (2002) PAUP*: Phylogenetic analysis using parsimony (*and Other Methods), Version 4.0b10, Sinauer Associates: Sunderland, MA, USA.

Tedersoo L, Bahram M, Põlme S, Kõljalg U, Yorou NS, Wijesundera R, Villarreal Ruiz L, Vasco-Palacios AM, Thu PQ, Suija A, Smith ME, Sharp C, Saluveer E, Saitta A, Rosas

M, Riit T, Ratkowsky D, Pritsch K, Põldmaa K, Piepenbring M, Phosri C, Peterson M, Parts K, Pärtel K, Otsing E, Nouhra E, Njouonkou AL, Nilsson RH, Morgado LN, Mayor J, May TW, Majuakim L, Lodge DJ, Lee SS, Larsson KH, Kohout P, Hosaka K, Hiiesalu I, Henkel TW, Harend H, Guo LD, Greslebin A, Grelet G, Geml J, Gates G, Dunstan W, Dunk C, Drenkhan R, Dearnaley J, De Kesel A, Dang T, Chen X, Buegger F, Brearley FQ, Bonito G, Anslan S, Abell S, Abarenkov K (2014) Fungal biogeography. Global diversity and geography of soil fungi. Science 346(6213): 1256688. https://doi.org/10.1126/science.1256688

Tohtirjap A, Hou SX, Rivoire B, Gates G, Wu F, Dai YC (2023) Two new species of *Exidia* sensu lato (Auriculariales, Basidiomycota) based on morphology and DNA sequences. Frontiers in Microbiology 13: 1080290. https://doi.org/10.3389/fmicb.2022.1080290

Vilgalys R, Hester M (1990) Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several Cryptococcus species. Journal of Bacteriology 172(8): 4238–4246. https://doi.org/10.1128/jb.172.8.4238-4246.1990

Wang S, Thorn RG (2021) *Exidia qinghaiensis*, a new species from China. Mycoscience 62(3): 212–216. https://doi.org/10.47371/mycosci.2021.03.002

Wang XW, May TW, Liu SL, Zhou LW (2021) Towards a natural classification of *Hyphodontia* sensu lato and the trait evolution of basidiocarps within Hymenochaetales (Basidiomycota). Journal of Fungi 7: 478. https://doi.org/10.3390/jof7060478

Weiß M, Oberwinkler F (2001) Phylogenetic relationships in Auriculariales and related groups – hypotheses derived from nuclear ribosomal DNA sequences. Mycological Research 105(4): 403–415. https://doi.org/10.1017/S095375620100363X

Wells K (1961) Studies of some Tremellaceae. IV. *Exidiopsis*. Mycologia 53(4): 317–370. https://doi.org/10.1080/00275514.1961.12017967

Wells K, Bandoni RJ (2001) Heterobasidiomycetes, In: McLaughlin DJ, McLaughlin EG, Lemke PA (Eds) The Mycota. (A Comprehensive Treatise on Fungi as Experimental Systems for Basic and Applied Research), vol 7B. Springer, Berlin, Heidelberg, 85–120. https://doi.org/10.1007/978-3-662-10189-6_4

White TJ, Bruns T, Lee S, Taylor J (1990) Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: Innis MA, Gelfand DH, Sninsky JJ, White TJ (Eds) PCR protocols: A guide to methods and applications. Academic Press, San Diego, 315–322. https://doi.org/10.1016/B978-0-12-372180-8.50042-1

Wijayawardene NN, Hyde KD, Al-Ani LKT, Tedersoo L, Haelewaters D, Rajeshkumar KC, Zhao RL, Aptroot A, Leontyev DV, Saxena RK, Tokarev YS, Dai DQ, Letcher PM, Stephenson SL, Ertz D, Lumbsch HT, Kukwa M, Issi IV, Madrid H, Phillips AJL, Selbmann L, Pfliegler WP, Horváth E, Bensch K, Kirk PM, Kolaříková K, Raja HA, Radek R, Papp V, Dima B, Ma J, Malosso E, Takamatsu S, Rambold G, Gannibal PB, Triebel D, Gautam AK, Avasthi S, Suetrong S, Timdal E, Fryar SC, Delgado G, Réblová M, Doilom M, Dolatabadi S, Pawłowska J, Humber RA, Kodsueb R, Sánchez-Castro I, Goto BT, Silva DKA, de Souza FA, Oehl F, da Silva GA, Silva IR, Błaszkowski J, Jobim K, Maia LC, Barbosa FR, Fiuza PO, Divakar PK, Shenoy BD, Castañeda-Ruiz RF, Somrithipol S, Lateef AA, Karunarathna SC, Tibpromma S, Mortimer PE, Wanasinghe DN, Phookamsak R, Xu J, Wang Y, Tian F, Alvarado P, Li DW, Kušan I, Matočec N, Maharachchikumbura SSN, Papizadeh M, Heredia G, Wartchow F, Bakhshi M, Boehm E, Youssef N, Hustad VP, Lawrey JD, Santiago ALCMA, Bezerra JDP, Souza-Motta CM, Firmino AL, Tian Q, Houbraken J, Hongsanan S, Tanaka K, Dissanayake AJ, Monteiro JS, Grossart HP, Suija A, Weerakoon G, Etayo J, Tsurykau A, Vázquez V, Mungai P, Damm U, Li QR, Zhang H, Boonmee S, Lu YZ, Becerra AG, Kendrick B, Brearley FQ, Motiejūnaitė J, Sharma B, Khare R, Gaikwad S, Wijesundara DSA, Tang LZ, He MQ, Flakus A, Rodriguez-Flakus

P, Zhurbenko MP, McKenzie EHC, Stadler M, Bhat DJ, Liu JK, Raza M, Jeewon R, Nassonova ES, Prieto M, Jayalal RGU, Erdoğdu M, Yurkov A, Schnittler M, Shchepin ON, Novozhilov YK (2020) Outline of Fungi and fungus-like taxa. Mycosphere: Journal of Fungal Biology 11(1): 1060–1456. https://doi.org/10.5943/mycosphere/11/1/8

Wijayawardene NN, Hyde KD, Dai DQ, Sánchez-García M, Goto BT, Saxena RK, Erdoğdu M, Selçuk F, Rajeshkumar KC, Aptroot A, Błaszkowski J, Boonyuen N, da Silva GA, de Souza FA, Dong W, Ertz D, Haelewaters D, Jones EBG, Karunarathna SC, Kirk PM, Kukwa M, Kumla J, Leontyev DV, Lumbsch HT, Maharachchikumbura SSN, Marguno F, Martínez-Rodríguez P, Mešić A, Monteiro JS, Oehl F, Pawłowska J, Pem D, Pfliegler WP, Phillips AJL, Pošta A, He MQ, Li JX, Raza M, Sruthi OP, Suetrong S, Suwannarach N, Tedersoo L, Thiyagaraja V, Tibpromma S, Tkalčec Z, Tokarev YS, Wanasinghe DN, Wijesundara DSA, Wimalaseana SDMK, Madrid H, Zhang GQ, Gao Y, Sánchez-Castro I, Tang LZ, Stadler M, Yurkov A, Thines M (2022) Outline of Fungi and fungus-like taxa – 2021. Mycosphere: Journal of Fungal Biology 13(1): 53–453. https://doi.org/10.5943/mycosphere/13/1/2

Wu F, Zhou LW, Yang ZL, Bau T, Li TH, Dai YC (2019) Resource diversity of Chinese macrofungi: Edible, medicinal and poisonous species. Fungal Diversity 98(1): 1–76. https://doi.org/10.1007/s13225-019-00432-7

Wu F, Zhao Q, Yang ZL, Ye SY, Rivoire B, Dai YC (2020) *Exidia yadongensis*, a new edible species from East Asia. Junwu Xuebao 39: 1203–1214. https://doi.org/10.13346/j.mycosystema.200205

Wu F, Tohtirjap A, Fan LF, Zhou LW, Alvarenga RLM, Gibertoni TB, Dai YC (2021) Global diversity and updated phylogeny of *Auricularia* (Auriculariales, Basidiomycota). Journal of Fungi (Basel, Switzerland) 7(11): 933. https://doi.org/10.3390/jof7110933

Wu F, Man XW, Tohtirjap A, Dai YC (2022a) A comparison of polypore funga and species composition in forest ecosystems of China, North America, and Europe. Forest Ecosystems 9: 100051. https://doi.org/10.1016/j.fecs.2022.100051

Wu F, Zhou LW, Vlasák J, Dai YC (2022b) Global diversity and systematics of Hymenochaetaceae with poroid hymenophore. Fungal Diversity 113(1): 1–192. https://doi.org/10.1007/s13225-021-00496-4

Yang Y, Li R, Liu CM, Zhao CL (2023) Morphological and molecular identification for two new species of wood-inhabiting macrofungi (Basidiomycota) from Yunnan-Guizhou Plateau, China. Phytotaxa 591(1): 1–18. https://doi.org/10.11646/phytotaxa.591.1.1

Yang Y, Li R, Jiang QQ, Zhou HM, Muhammad A, Wang HJ, Zhao CL (2024) Phylogenetic and taxonomic analyses reveal three new wood-inhabiting fungi (Polyporales, Basidiomycota) in China. Journal of Fungi (Basel, Switzerland) 10(1): 55. https://doi.org/10.3390/jof10010055

Ye SY, Zhang YB, Wu F, Liu HX (2020) Multi-locus phylogeny reveals two new species of *Exidia* (Auriculariales, Basidiomycota) from China. Mycological Progress 19(9): 859–868. https://doi.org/10.1007/s11557-020-01601-8

Zhang XC, Li YC, Wang YY, Xu Z, Zhao CL, Zhou HM (2024) *Xylodon asiaticus* (Hymenochaetales, Basidiomycota), a new species of corticioid fungus from southern China. Phytotaxa 634(1): 1–15. https://doi.org/10.11646/phytotaxa.634.1.1

Zhao CL, Wu ZQ (2017) *Ceriporiopsis kunmingensis* sp. nov. (Polyporales, Basidiomycota) evidenced by morphological characters and phylogenetic analysis. Mycological Progress 16(1): 93–100. https://doi.org/10.1007/s11557-016-1259-8

Zhao CL, Qu MH, Huang RX, Karunarathna SC (2023) Multi-gene phylogeny and taxonomy of the wood-rotting fungal genus *Phlebia* sensu lato (Polyporales, Basidiomycota). Journal of Fungi (Basel, Switzerland) 9(3): 320. https://doi.org/10.3390/jof9030320

Zhao H, Wu YD, Yang ZR, Liu HG, Wu F, Dai YC, Yuan Y (2024) Polypore funga and species diversity in tropical forest ecosystems of Africa, America and Asia, and a comparison with temperate and boreal regions of the Northern Hemisphere. Forest Ecosystems 11: 100200. https://doi.org/10.1016/j.fecs.2024.100200

Zhou HM, Gu ZR, Zhao CL (2024) Molecular phylogeny and morphology reveal a new species of *Asterostroma* from Guizhou Province, China. Phytotaxa 634(1): 1–15. https://doi.org/10.11646/phytotaxa.640.1.1